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P. KURITUK M. MUTALUH M. DURITUK. TORIGON K. TANIMOTO T.,
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15-JUL-1998 (REL. 35, LASI ANNOTATION UPDATE)
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L: U68701; G2228534; -.
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22326 MW:
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Pred. No. 1.3e-28;
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22: Indels

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SCIENCE 259
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ACT_SITE
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ATP-DEPENDENT PROTEASE LA (EC 3 4 21.53)
LON OK LON'A OK HT0462.
HAEMOPHILUS INFLUENZAE
EROPERSPORT
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PROSITE: PSONIO46: LON_SEP: 1
HYDROLASE: SERINE PROTEASE: AID-BINDING
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CAPALLYIC ACTIVITY HYDROTYSIS OF LAPGE PROTEINS SUCH AS GLORIN, CAPALLYIC ACTIVITY SERVIN ALBUMIN, IN PRESENCE OF AITP CASELIN AND CHARTEFATED SERVIN ALBUMIN, IN PRESENCE OF AITP
                                                     SCROFA (PIG).
AFYSTA METASSA
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STRUCTURE TO CATION: CYTICFLASMIC,
SIMILARITY: RELOWS TO PEPTITIASE FAMILY S16; ALSO KNOWN AS
LON FAMILY OF AIP-DEPENDENT PROTEASES.
L; U22729; C1573440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -SEQTRLIIEMYKDSE-------VEGLAVTLSVKDSKMSTLSCKNKIISEE 83
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                                                     VERTERRATA, TETRAPODA; MAMMALIA;
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         2ABA_YEAST
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Best Local Similarity
Matches 27; Conserv
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Q00362;
01-APK-1993 (REL. 2
01-00T-1996 (REL. 2
01-NOV-1997 (FEL. 3
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01-00T-1996 (MEL. 34. LAST SEQUENCE UPDATE)
01-NV-1997 (MEL. 35. LAST ANNOTATION UPDATE)
PROTEIN PROSPRATASE PPZA REGULATORY SUBUNITY
CONTROL PROTEIN 55).
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MEDLINE, 93314975.

HURTHER M.J., LIN G., SMITH D.M., MURIAUGH M.F., MULLIOR T.W.,

TENNETICE, 129-1299(1993).

7ENET 129-1299(1993).

7ENET 129-1299(1993).

THYMOCYTE PROLUCEL BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

THYMOCYTE PROLUCEL BY ACTIVATED MACROPHAGES, B-CELL

MATURATION A PROLUFFRATION BY INCUCING IL-2 RELEASE, B-CELL

MATURATION A PROLUFFRATION, & FIRECHARMATORY PREPONNER, BRING

ITENITEDER ARE INVOLVED IN THE INFLAMMATORY PREPONNER, BRING

ITENITEDER ARE INCUCENCE PROSENCE, AND ARE REPORTED TO STIMULATE

THE RELEASE OF PROSTAGLANCIN AND COLLAGENASE FROM SYNOVIAL CELLS
                                                                                                                                                                                                                                                                                                                                                                                       MECLINE: 92917858.
HEALY A.M., ZOUNIEROWICZ S.
DEPAOLI-ROACH A.A., DPINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDC55 OF YGL1900 OF G1345.
SACCHARUMYCES CEREVISIAE (BAKER'S YEAST)
                                                                                                                                                                               BRUSCHI C.V.;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
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THE SIMILARITY AMONG THE JI-1 PRECIPEOPE ENGGESTS THAT THE AMIXENIS OF THESE PROTEINS SERVE SOME AS YET UNLESS FUNCTION.
THE LACK OF A SPECIFIC HYLMOPHOBIC SEGMENT IN THE PRECIPEOR SEQUENTE SUBJECT THAT HE IS RELEASED BY DAMAGED OFFICE OR IS SECRETED BY A MECHANISM DIFFERRUM FROM THAT USED FOR OTHER
FUNCTION: PHOSPHAIASE ZA AFFECIS A VARIETY OF BIOLOGICAL PROCESSE. IN THE CELL STORM AS TRANSCRIPTION, CELL CYCLE PROSPESSION AND CELLULAR MORPHOSENESIS, AND PROVIDES AN UNITIAL IDENTIFICATION OF CHILCAL SUBSTRATES FOR THIS PHOSPHATASE. THE RESULT AND VERLAPPING. MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT CVERLAPPING.
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INE: 97197971
JEVINA M / KITMA E
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FN0724; JN0724.
                                                                                                                                                      13:55-64(1997)
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                                                                                                                                                                                                                                                                                                                                                           NIEROWICZ S., SIAPLETON
A. DPINGLE J.R.;
. 11:5767-5780(1991).
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CH SEEN
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BELA EXHIBATES.

WONTS BELA EXISTS IN SEVERAL ERINGRIC FORMS, ALL OF WHICH NATES FOR A STREET IMPOSES OF A CATALYTIC SUBUNIT ASSOCIATED WITH NATES OF A STRUCK (1985) (SHRINIT A) THE CORE COMPLEX A GASSIANS WITH A THROP, VARIABLE SUBUNIT (SUBUNIT B), WHICH NEEDS STEENER THE HOLDENZYME.

MICHAELT LEW MO. WITH STHER SPECIES PHUSCHATASE ZA REGULATORY PURITY B.
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"HEM. RI PHYJ. RES. COMMUN. 188:1273-1279(1992).
HINCT: M. THE NEWFOXET COMPONENT IS NECESSARY TO MAINTAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOOSS TENDED TO YMYKOTERNATIAN -- TISVKOSKMSTISCKNKTISFFEMDPPEN-- 91
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        LOSS DESCRIPTION OF STREET OF STREET STORE
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                                                                                                                                                      TOTOTOSTO TERMENAVIONNEMERROST YEORET ACOMETIVALE 193
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1 ML+101 TRO12;
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MEDITINE, 96837-99 (MET 5 MO). SECULIVE, PROSCHEMIN R.D., PROSENDE L.M., CLAYER R.D., DECEMBERY B.A., FORESENED L.M., CLAYER R.D., REICH C.T., KEPLAVAGE A.E., DECEMBERY B.A., 100MB J.-F., ADAMS M.D., REICH C.T., WEBPREFY F., EIRKRESS E.E., WEIRKRESCY F.G., MERBYRE T.M., MILER M. COTTON H.D., ROBORDAGEN N.S.M., WEIRMAN J.F., FUHPMANN J.T., NOUVEN G.T.TEFRANY T.B., REICHY J.M., PETERSON J.E., SALAW F.M., HANDA M.C., TOTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.D., BORDOVSKY M., VEINK B.-P., FRASEP C.M., SMITH B.D., WEEE C.R., VENTER J.C., MILOSTO, M.D., SOLICIOS 10 THE M.JANNASCHI M.T.S.C., MILOSTO, MILOSTO, M.T. SALAKILY, ELECTRIS 10 THE M.JANNASCHI M.T.S.C., MILOSTO, M.T. SALAKILY, M.T. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1998 (FEI 10, CHEALL)
01-MAR 1989 (REI 10, LAST SEQUENCE UPDATE)
01-NOV-1995 (PEL 32, LAST ANNOTATION UPDATE)
INTERTEURIN-1 PETA PERCUPSOR (IL-1 BETA).
LEONS S.F., FLAGGS G M., LAWMAN M., GE
NUCLEIC ACIDS RES. 16:9054-9054(1988).
[2]
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EMBL: U67525: G1499632; -.
TIGR: MJ0809: -.
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01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE: 89016591.
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EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAI
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ilarity 26.8%: Pred. No. 1.6;
Conservative 17; Mismatches 78.
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                                                                                                                                                                    CRAY P.W.:
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Best Land &
Matches 32
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MEDICINE: RSC61882
LOMEDICO P.T., GURTER H
FAN Y.-CLE., COLLIER K S
PAN Y.-CLE., COLLIER K S
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01 007-1986 (REL 34
1NTERFERMIN-1 ALEBA
                                                               J. BIOL.
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P01582:
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                                                                                                      PHUSEHURYLATION AT SER-90.
MEDLINE: 88153709.
PETISCHER H TI NICKELLS M
                                                                                                                                                                                                                                                                                                                                                                                                  MUS MUSCULUS (MOUSE)
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MEDLINE, 88318
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SYMILARITY: BELONGS TO THE IL-1 FAMILY.
L: M35589: G133C3; -.
L: X12498 G449: -.
T- M3721: G164201 -.
TJL0010: TCR01B
SCHEP H. NICKELLS M.W. COLTEN H.P.:
BIOL. CHEM. 263.4023.4028(1982).
FUNCTION: PROFUCED BY AGITVATED MACPOPHAGES, IL-1 STIMULATES
THYMOCYTE PROFUCED BY AGITVATED MACPOPHAGES, B-CELL
MALURATION & PROFUTERPATION BY INCOCING IL-2 RELEASE, B-CELL
MALURATION & PROFUTERPATION, A FIREOPHAST GROWTH FACTOR ACTIVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: MONOMER.

THE SIMILARITY AMOND THE IL-1 PRECURSORS SUGGESTS THAT THE AMIND ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

THE LACK OF A SECTIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SHOWESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OF IS
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FOUNTION PROGRACED BY ACTIVATED MACEPOPHARES, IL-1 STIMULATES
THYMOCYTE PROLIFERATION BY INDICING II-2 RELEASE, B-CELL
MATURATION & PROLIFERATION & FIBROBLAST GROWTH FACTOR ACTIVITY
IL-1 PROTEINS ASE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
TORNITETED AS ENDOGRADORS PROPRISED, AND ARE REPORTED TO STIMULATE
THE RELEASE OF PROGRAMANIAN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECRETFO BY A MECHANISM DIFFERING FROM THAT USED FOR CIREP
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901584: THIE:
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L. 61 (AST SECHEN'E HPDATE)
L. 34. LAST ANNOTATION GEDATE)
This drecursor (That Alpha)
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Best Local &
Matches 31
                                                                                                                                                                                                                               ENTIAN K -D. KOETTER D. POSE M. RECKER J. GRRY W. 11.2., MIEGERANN E., SCHENK-GROENINGER R., SERVOS J. WEHNER E., WOLTER R. SERVOS J. RRAUN H., DEFN K. DUESTERHUS GRUENNEIN R., HEDES E., KIESAU P., KOROL S., KREMS B., FROET STEGERS K., RAUR A., BOLES E., MIOSGA T., SCHAARF-GERSTENSCHLARGER I., ZIMMERMANN E.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-07-1994 (REL 30, CREATER)
01-07-1994 (REL 30, LAST SEQUENCE OPDATE)
01-00V-1997 (REL 35, LAST ANOTHTION UPDATE)
HYPOTHETICAL 79.2 KE (ESTEIN IN EREF-COSTS INTERCLATE REGION THRESPORTED TO THE REPORT OF THE RESIDENT TRANSPORTED TO THE RESIDENT TRANSPORTED TO THE RESIDENT TRANSPORT
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PPOSITE: PS00253; INTERLEUKIN_1; 1.
CYTOKINE: MACEGEHAGE: MITGGEN: INFLAMMATORY FESDONSE; RYFCGEN;
                                                                                                                                                                                                                                                                                                                  STEAIN SCEEC, KOETTER D.
ENTIAN K -D. KOETTER D.
NIEGEMANN E., SCHENK-GRO
                                                    2 IMMERMANN F.K.;
                                                                       MEDLINE: 93255907.

BAUE A , SCHAAFE OFFSTENSCHLAEGER
                                                                                                                               STRAIN-S288C
                                                                                                                                                       SEQUENCE FROM N.A.
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EUKARYOTA: FUNAI; ASCOMYCUTINA: HEM(ASCOMYCETES
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THE SIMILARITY AMONG THE II-1 PRECINSORS SUGGESTS THA: THE LENG OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION THE LACK OF A SPECIFIC PROPORHORIC SEGMENT IN THE PRECIPSOR SEQUENCE SUGGESTS THAT II-1 IS RELEASED BY LAMAGED CELLS OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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NOV *** (BELL 16, LAST SKUDERUE UPDATE)

NOV *** (BELL 42, LAST ANNOTATION UPDATE)

NIERLE KIN ** ALTHAN PREPRIESSP (IE-) ALPHA).
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FUNCTION OF PRICED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
HYM N.F. WHIFERATION BY INJURING IL-2 RELEASE, B-CELL
HYM N.F. WHIFERATION BY INJURING FOR MACHINE FACILIF ACTIVITY
HATUGAL WITH A REINFORMATION OF REPORTED TO STIMULATE
DENTIFIED ALL ENDOLPHING HYROGEN, AND ARE REPORTED TO STIMULATE
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                                                                                                                                                                                                                                                              ENDS : THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
HIG LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
BROWNESS SECRET IN 1 IS RELEASED BY DAMAGED CELLS OR IS
BOOKET BY A MEDIANISM DIFFERING FROM THAT UNEF FOR OTHER
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                                                                                    PARK TRADU, MIRRORN INFLAMMAINAY KESPONSE, PYPOJEN
                                                                                                                                                                                                                                          SNIEL SELNS
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FOTENTIAL.
FOTENTIAL.
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Pard No. 1
N \rightarrow I (IN REF. 2).
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                                                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.5%; Score 77.5; DB 1: Length 439; Best Local Similarity 23.7%; Pred. No. 7.3; Matches 37; Conservation 26; Mismatches 46; Indexs 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BULT C T, WHITE O. OLSEN G J. ZHOU L., ELEISCHMANN R.D.,
SUTTON G.G., RIAKE J.A., FITZGERALD L.M., CLAYCON B.A., GOCAYNE J.D.,
KERLAVAGE A.B., DOUGHERTY B.A., TOMB J.-E., ADAMS M.D., REICH C.I.,
OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERBICK J.M., GLOTEK A.,
SCOTT J.L., GEOGHAGEN N.S.M., WILLMAN J.E., FUHERMAN J.L., NGTYEN I.
UITEBRACK I.K., KELLEY J.M., PELERSON J.D., SALOW P.W., HANNA M.C.,
COTTON M.D., POPERTS K.M., HUPST M.A., KALNE B.P., BOPGDOVSKY M.,
KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;
SCIENCE 73:1058-1073(1996).
--- SIMILABITY: 10 M. JANNASCHII MJ0977 AND SOME, TO ELOCAL VIEM.
EMBL. 1577-25, 31432634; -.
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01-NOV-1997 (PEL. 35, CPEATED)
01-NOV-1997 (REL. 35, LAST SEO!
15-JUL-1998 (PEL. 36, LAST ANN-
HYPOTHETICAL PROTEIN MJ0811.
HTPG_HELPY
P56116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96337999.
BULT C T ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROIEIN. SECUENCE 4:9 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR: MJ0811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METJA
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                                                                                                                                                                                                                                                                                                                113 FE-----SSLYEG-------HFLACQKEDDAFK 133
                                                                                                                                                                                                                              332 FUETIELIASLYFGGGINFIMPLNRAMSLIKEHETFK 367
                                                                                                                                                                                                                                                                                                                                                                                        297 DREIWCKAVALSI----TEIAFFENFDIYYIAFD......
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 VTLRISHTRI: FVSAQNEDEPVILKEI PETEKTIKDETSILIPEWEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 DSEVPGLAVILSVKDSKMSILSCKNKIISFEEMDPPENIDDIQSDLIFFQKRVPGHNKME 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 VILSVKDSKMSTISCKNK+++IISEPEMI-PPENIDDIQSOLIFFOFFVFOHNEME-FESS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
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27∪ AA:
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                                        STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DSM 2551 / A100 43057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE MW: OF START CHC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUZBB MW;
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                                        PRT:
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Search completed: June 22, 1999, 10:59:48 Job time: 74 sec
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                                                                                                                                                                                                                                                                                                                                                         Query Match

9 4%; Score 76.5; DB 1; Length 621;

Rest local Similarity 23.2%; Fred. No. 13;

Matches 09 Observative 27; Mismatches 52, Indels 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOMB I -F. WHITE O. KFFLAVAGE A P. CLAYTON P A., SUTTON G.G., FLEISCHMANN P N. KFFLHUM K A. KLENK H -P., GILL S., DOUGHEPPY B A., NELSON K . "CACKNINGS I ZHOUL KIPKNESS E F. PETERSON S., LOFIUS B. FICHARUSON D. LODSON P, KHALAK H G., GLOEK A., MCKENNEY K., FITZGERALD L.M., LEE N. ADAMS M. D. HICKEY E K., MCKENNEY K., FITZGERALD L.M., LEE N. ADAMS M. D. HICKEY E K., MCKENNEY K., FITZGERALD L.M., FULL C., BOMMAN C., WAITHEY L., WALLIN E., COTTON M. D. WEITMAN J. M., FULL C., BOMMAN C., WAITHEY L., WALLIN E., COTTON M. D. WEITMAN J. M., FULL C., BOMMAN C., WAITHEY L., WALLIN E., COTTON M. D. POPODOVSKY M., KAPP P. D., SMITH H.O., FRASER C.M., VENTER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGE: HP0210; -.
PROSITE: PS00298; HSP90; 1.
PROSITE: PS00298; HSP90; HEAT SHOCK.
CHAPERONE: AIP-BINDING; HEAT SHOCK.
SECUENCE 621 ZA; 71274 MW, 234A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
HTPG OR HP0210.
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(BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

EMBL. AEC(0541) G2313300; -.
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NATURE 388:539-547(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HELICOPACTER PYLORI (CAMPYLOBACIEK PYLORI).
PROWARYGIA: GEACILLOUIES; SCOTOBACTERIA;
AERORIC, MOTILE, HELICAL AND/OR VIBRIGID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 97394467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=26695;
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                                                                                                          144 NSDQA 148
                                                                                                                                                  142 NGDKS 146
                                                                                                                                                                                       61 EHLGTIAKSGTKNELSALSGDKKKDSALIGQEGVGEYSAEMVAS-----KIVVQTKKV 143
                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                         31 LPELVSNASDALDKINVIMITDEKIKGINTTPSIHISFDSQKKTITIKDNGIGNDKNDII 90
                                                                                                                                                                                                                                                                                                               32 MIDID, SASEDQIRCIIYMYKDSEVRGLAVILSVK---DSKMSTLSCKNKIISFEEMDPP 88
                                                                                                                                                                                                                                 ENIDD: -2SDLIFFQKRVPGHNKM-----EFESSLYEGHFLACQKEDDAFKLILKKKDE 141
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GenCute Persion 4.5

Copyriain GenCute Persion 4.5

For a Tiber Process Search using sw model

For a Tiber CS-09-030-061-1

Sequence CS-09-030-061-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by modified. If the total score distribution

## SUMMARIES

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SECURENTE FROM N.A. SECURENTE FROM N.A. STRAIN-SEPAGUE DAWLEY: TISSUE-WHOLE BRAIN: CULLINE A.C., HALL M.D., ROTHWELL N.J., LOHESHI G.N.: "Choning of rat brain interlockin-18 cDNA."; M.A. PSYCH. K. 657-266(1986). EMEL. A.T222813; E1335191;	INTEREDUALN-18. IL-18. RAITUS NGEVEGIGUS (BAT). RUKARYUIA, METAZUA, CHURDATA, VERTEBEATA; MAMMALIA; BUTHERTA; RUPENTTA, SCIURORNATHI; MURIDAE; MURINAE; BATTUS.	1998 (TERMELPEL 08, GREATED) -1998 (TERMELEEL 08, LAST SECONDER OF LAST ANNO	RESULT 2 088749 ID 088749 EPELIKINARY: PRT; 194 AA.	1 NEQULE 6	Query Match Best Donal Similarity 100.09: Score 31, DB 2, Locath 193: Matches 6, Topechatine C, Mismatches 0: Indois C: Gaps

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AND SNE C. SCHEETT
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*** (ISEMMUREL 92, LAST SEQUENCE UPDATE)

*** (ISEMMUREL 92, LAST ANNOTATION UPDATE)

EC BOSSA TO 877 892 (SECTION 75 OF 400) OF THE COMPLETE GENOME
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AL, GENRAMF, GERBE DATA BARKT
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Score 26: DB II: Length IIO: Stod. No. 12: Conditional des Co. Indels
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Prod. No. 4.4;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIR-BRIGHTON:
MEDITINE: 94233741.
MEDITINE: 94233741.
"Identification of binding sites for neutralizing memoricual authorises on the 14 kbg fasion protéin of orthopox viruses:
WIROLOGY 200:778-783(1994).
EMBL: X75158; G404264 - .
SEQUENCE 110 AA: 12514 MW: 41830309 CFC32:
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MEYER H., OSTERRIEDER N., CZERNY C.P.;

"Identification of binding sites for neutralling monoclonal antibodies on the 14 the distinct protein of orthopox viruses.";

VIROLOGY 200:778-783(1994).

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SPQUENCE 117 AA: 13316 MW: 789E8251 CPC32:
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01-NOV-1998 (TREMBLREIL
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01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
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                                                                                                                     Pred. No. 12:
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RN SECTION G. G. SLARE J.A. FITZESPALE L.M. FLETSCHMANN R.D., REICH G.I.,

PA BULL O' MHITE O. OLSEN G.J., ZHOU L., FLETSCHMANN R.D., REICH G.I.,

PA SUTTON G.G. SLARE J.A. FITZESPALE L.M. GARANS M.D., REICH G.I.,

PA CVERBEER F., FOUGHERTY P.A. TOMB J.-F., ADAMS M.D., REICH G.I.,

PA CVERBEER F., KIFKNESS E.F., WEINSTLAN E.G. MEFLEY T.V. CLORY A.,

PA CUTTON M.D., FOUGHERY J.M., PETERSON J.D. SADOW P.W., HANNA M.G.,

PA CUTTON M.D., FOUGHER S.M., HUPSI M.A., RAINE B.F., BUFFLEVSKY M.A.

COUTTON M.D., FOUGHER S.M., HUPSI M.A., RAINE B.F., BUFFLEVSKY M.A.

PA KLENK H.-P. FRASER C.M., SMITH H.O., WOESE C.P., VENTER J.G.;

TOSMPAUCH GROWNE SEQUENCE OF THE MECHANOGERIC ARCHAROLIST IN STREET TOMBOOK STATES TO CLASS-II AMINOACYL-TENA SYNTHETASES.

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DR EMBL: U67553: G1591750; -.

DR EMBL: U67553: G1591750; -.
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CO1641:
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ENGSITE, FS00990, CLAILADAFIOR_M_1; 1.
PROMITE: PS00991; CLAILADAFIOR_M_2; 1.
PRAM, PF00928; Adap_comp_sub; 1.
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EUKARYOTA: METAZOA; ARTHROPODA; TRACHEATA; HEXAPODA; INSECTA;
PIERYGOTA; DIPTERA: EPACHYCEKA: MUSCOMOPPHA: EPHYDROIDEA;
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ALL".

THE SOPH A MELAN-GASTER (FRUIT FLY)

CTEARYC A. MELAZ A. AKTHROPODA; TRACHEATA; HEXADODA; INSI

CTEARYC A. MELAZ A. AKTHROPODA; TRACHEATA; EFHYDROTDFA.
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1870-3168A, SERONGODEA: SPRINGIDAE, SPRINGINAE, MANDUCA
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AN ARTHRETE NAN TRACHEATA, HEXARGEA, INSECTA:
RITHRA: SHHINNINODRA: SPHINNIDAE; SPHINGINAE; MANDUCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAT ABABT RUMETT TO
TAT AFABTOR MUZO TO
1 4991 MW: ZARTOZD CRCTZ:
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                                                                   ARTHROGODA: TRACHEATA: HEXAPODA: INSECTA
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87.88; Prod. No. 12;
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91. (AST SPOMENCE MEDIATE)
99. (AST ANY STATION MEDIATE)
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Fred. No. 91;
I: Mismatches u: Indels
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017901 PRELIMINARY: PRT: 1763 AA.
Q17901: Q20887;
01-NJV-1996 (TREMBUREL, 01, CREATED)
01-NJV-1998 (TREMBUREL, 08, LASI SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Ouery Match 87.1%;
Best Local Similarity 83.3%;
Matches 5; Conservative
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WILSON B. AINSCOUTH F., ANDERSON E., BAYRES C., BERNA M., BORFIELL I., BURTON T. CONNEIL M. CORREY J. CORREY J. CORREY D. CARANTON M.
DEAR S., ED Z., DURBIN E., FAVELLO A., FULLON L., GARDINEK A., GREEN F., BIAMFINO T., BILLER L., JIER M., JARREION C., MES M., LASSER N., LATRELLE P., LIGHTNING J., LIOYD C., MCMITRAY A., MORTIMORE B., C'CALLAGHAN M., PARSONS J., PERCY C., MCMITRAY A., MORTIMORE B., C'CALLAGHAN M., PARSONS J., PERCY C., SCHWIRERY E., STADEN R., SULSTON J., THIBERY-MIEG J., THOMAS K., SONNHAMMER B., STADEN R., SULSTON J., THIBERY-MIEG J., THOMAS K., WALLKINSON-SPROAT J., WOHLDMAN P., WILKINSON-SPROAT J., WOHLDMAN P.,
                                                                                                                                                                                                   NATURE 368:32-38(1994).
EMBL: 783115; E31527; -...
PEAM: PEONG28; Adapt comp_sub; 1.
SEQUENTE 425 AA: 48842 MW: 2
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EUKAPYOTA: METAZOA: NEMATOFA: SFCEPNENTEA: EHABDITIA: EHABDITIDA:
EHABDITINA. EHABDITOIDEA, EHABDITIDAE, FELODEKINAE: CAENOFHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TREMBLREL, 04, GREATED)
01-JUL-1997 (TREMBLREL, 04, LAST SEQUENCE UPDAID)
01-JUL-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
K11D2.3.
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EMBL: U58861; G1378131; 1.
PPAM: PFU0079; Serpin: 1.
ETGCTECT 475 AA. 1-484 MW. ITTABESE CHOSE:
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MEDLINE: 97067009.

JIANG H.: MANG Y.: MULNIX A.B.: KADE: J.: 101E K.:

JIANG H.: MANG Y.: HUANG Y.: MULNIX A.B.: KADE: J.: 101E K.:

KANDS! M K.:

"Organization of serpin gene-1 from Manduca sextial Evolution of
                                                                                                                                                                                                                                                                                                                                                   "2.2 Mb of contiguous burleytide sequence from chromosome fit of coelegans.";
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Local Similarity 83.3%; hes 5. Conservation
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    Mismatches

                                                  Score 27; DB 3; Length 425; Pred. No. 90;
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Search completed: June 22, 1999, 11:01:19 Job time: 165 sec
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Best Local :
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MEDLINE; 9:150718.

WILSON R. AINSCOUGH P. ANDEPSON K., BAYNES C., BERKS M., BONFIELD J.,

BUBTION T. CONNELL M., CORREY F., COURSON A., CRAXTON M.,

BURTON T. CONNELL M., CORREY F., COURSON M., GREEN P.,

PARKTYS T. HILLER I., JIEP M., JOHNSTON L., JONES M., KERSHAW J.,

KIRSTEN T. I LAISTEP N., TATREILLE P., LIGHTNING J., LLOYD C.,

KIRSTEN T. HILLER R., C'CALLAGHAN M., PARSONS J., PEPCY C.,

MUNUPRAY A. MOPTIMORE B., C'CALLAGHAN M., PARSONS J., PEPCY C.,

MUNUPRAY A. MOPTIMORE B., C'CALLAGHAN M., PARSONS J., EDCY C.,

MUNUPRAY A. SAUNCEPS D., SHOWNKEEN R., SMALDON N., SMITH A.,

SONNHAMMER E., STADEN R., MATISON A., WEINSTOCK L.,

WILKINSON-SPECAI J., WOHLDMAN P.,

WILKINSON-SPECAI J., WOHLDMAN P.,

WILKINSON-SPECAI J., WOHLDMAN P.,

WILKINSON-SPECAI J., WOHLDMAN P.,

10.2.2 Mb of contiquous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans.";

MATURE 368:32-38(1994).

EMBL: 269211: E1321758: -

EMBL: 269662: E1321758; JOINED.

EMBL: 269662: E1322536; -

EMBL: 269662: E1322536; -

EMBL: 269662: E1322536; -

EMBL: 269662: E1322536; JOINED.

EMBL: 269662: E1322536; JOINED.
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5: Conserv
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83.3%;
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Fred. No. 4.le·02;
l; Mismatches 0;
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             protein search, using sw model
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3.566 Million cell updates/sec
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p43980 haemophilus p202747 mycoplasma p22747 mycoplasma p23585 mus musculu p35602 caenorhabdi p35585 mus musculu p35602 caenorhabdi p35585 mus musculu p36920 bacillus ci p14014 bacillus ci p14014 bacillus ci p14014 bacillus ci p14014 bacillus sp p23747 breumovysti p207474 bacillus ci p1604874 breumovysti p207474 breumilus p1605855 triticum ae p37825 oryau sative p207474 breumovysti p1604774 breumovysti p1797675 syrpechosyst p16466 mus musculu p23816 variola vir p16466 mus musculu p16466 homo sapien p16466 mus musculu p16466 homo sapien p16466 homo sapien p16466 mus musculu p16466 homo sapien p16466 mus musculu p16466 homo sapien p16466 mus musculu p16466 homo sapien p1646735 syrpechosyst p57321 alcaligens
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Matches of Conservative
TISSUE-LIVER:
MEDLINE, ACUCLU9.
OKAMMERA H., TSHTUI H
TANIMOTO T., TORIGUE
                                                                                                                                                                              LMOUSE STANDARD, PRT: 192 AA.

ILL8_MOUSE STANDARD, PRT: 192 AA.

P70380;

15-JML-1948 (PRI -4, CREALED)

15-JUL-1948 (REL 36, LASI SEQUENCE UPDATE)

15-JUL-1948 (REL 36, LASI ANNUANICH UTDATE)

17-JUL-1948 (REL 36, LASI ANNUANICH UTDATE)

17-JUL-1948 (REL 36, LASI ANNUANICH UTDATE)

17-JAMA-LMOUTHY FACTIF, (THIEFLETZIN-1 JAMMA), LL 1 JAMMA, LMOUTHY FACTIF, (THIEFLETZIN-1 JAMMA), LMOUTHY FACTIF, LMOUTHY FACTIF, (THIEFLETZIN-1 JAMMA), LMOUTHY FACTIF, LMOUTHY FAC
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ILIA_HHMAN STANDARD: PRT: 193 AA.

Q14116;
15-JUL-1948 (REL 36, CREATED)
15-JUL-1948 (REL 36, LASI SEQUENCE OPLATE)
15-JUL-1948 (REL 36, LASI SEQUENCE OPLATE)
15-JUL-1948 (REL 36, LASI ANNOTATION UPDATE)
15-JUL-1948 (REL 36, LASI ANNOTATION UPDATE)
17-JUL-1948 (REL 36, LASI ANNOTATION UPDATE)
17-JUL-1948 (REL 36, LASI ANTOTATION UPDATE)
(IFN-GAMMA-INCOULNG FACTOR) (INTERLEGENNA) (IL-1 GAMMA).

ILB OR TGIF.
10-MO SAPIENS (HUMAN).

FUTARFY (A. METATIA, THE STATA, VERTEBRATA, ILLESALLA, PAMMALLA).

EUTHERTA: PRIMATES.
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CHAIN
SEQUENCE
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ILSSUE-PERFERENT BLOUD;
CONTI B. KIM S.J. IN IMMC, DERWARK, TERT EATA BANKS.

--- PUNTIEN ANDMENIS NATURAL FILLER CELL ACTIVITY IN SIGLED CELLS
AND STEMPLATES INTERFEREN GAMMA FERICOTIEN IN I BOLLOS TUPE I
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USHIO S. NAMBA M., ORUPA T., HATTOFF K.,
TANABE E., EONIGHI K., MICALLEF M., EUJII
EUKUDA S., IKEDA M., CKAMURA H., KURIMOTO
J., IMMUNOL. 156:4274 4279(1996).
                                                                                                                                                           MUS MUSCULUS (MOUSE).
                                                                                           SEQUENCE FROM N.A..
                                                                                                                                         EUIHERIA; RODENTIA.
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  MORADA Y.,
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M., TORIGOE K., TANIMOTO
M.:
  HATTORI
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P43980;
01-NOV-1995 (REL. 32, CREATED)
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01-00T-1994 (REL 30, LASI SEQUENCE UPDATE)
01-NOV-1995 (REL 32, LAST ANNOTATION UPDATE)
LACITETN 481, LACIOCOCCIN BIOSYNTHESIS PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTI B., JAHNG J.W., TINTI C., SON J.H., JOH T.H.:
J. BIOL. CHEM. 272:2005-2007(1997).
-1- FUNCTION: AUGMENIS NATURAL KILLER CELL ACTIVITY IN SPLEEN TELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.00 (MAN (FIL M. LAN) SELIENTE INTALE)
15-JUL-1998 (REL R6. LAST ANNOTATION UPDATE)
INTERLEUKIN-18 PRECUESOR (IL-18) (INTEREFERON-GAMMA INDUCING FACTOR)
(IEN-GAMMA-HUDGGING FACTOR) (INTERLEUKIN 1 GAMMA) (IL-1 GAMMA).
IL18 OR IGIF.
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PINCE A . EUROUR A . TE POSAM S., THUMULI E.,
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FÜNCIION: COULD BE IMPLICATED IN THE PROCESSING SETERCORES OF THE LANTIBIUTIC LACTICIN 481/LACTOROLINEL; U04057; G433322; -.
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PROSTIE: PROCEAR: INTEGRIN_BETA 2.

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PROSTIE: PRO1186: EGE_2; UNKNOWN_1.

THEORY: CEIT ACHESTIN TRANSCEMPANE 3IA
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GLYON
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01-MAY 1992 (REU. 22. GKEALEU)
01-MAY 1992 (REU. 22. LAST SECUENCE UPDATE)
01-MAY 1994 (SEC. 26. LAST ANNOTATION REDATE)
INTESRIN BETA-8 SUBUNIT PRECUPSOR
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1- S.MILARITY: STRONG, TO E.COLIENCE: 92271; G1672273; -.
TIGR: H10304; -.
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LE M., MAPIER M.A., MCLEAN J.W.,

LE M., MAPIER M.A., MCLEAN J.W.,

FUNCTION 255:19458-19458(1991).

FUNCTION AS SECEPTIAS FOR SELL ACHESION MCLECULES.

FONCTION AS SECEPTIAS FOR SELL ACHESION MCLECULES.

STRENGTT STORE OF AN AIPHA AND PETA STRUNKT RETA-8 ASSOCIATES
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THESE SEPCIFICITY PLACENTA VILNEY RRAIN OVAR
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_MYDC_MYCKE STANDAPD: PRT: 1052 AA.

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P.2747, 24448], 243482, 14424, 243385, 2492

01-AUG-1991 (REL. 19, CREATED)

01-AUG-1991 (REL. 19, LASI SEQUENCE UPDATE)

01-MOV-1997 (REL. 35, LASI ANNOTATION UPDATE)
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MEDLINE 92051996 / G 37:

MEDLINE 92051996 | BETERSON S.H. SCHERAMM H., HC F.-C. B.

NCCLEIC ACIDS KES. 19.6027-6031(1991).

EMBL. M:1431 | G150160; T.

EMBL. B:4545 | TJATP77 | .

EMBL. 902124; G409890; T.
                                                                                                                 MEDLINE: 94975230.
PETERSON S.N., HU P.-C., BUTT K.F
J. BACTERIOL. 175:7918-7930(1993)
                                                                                                                                                       SERVENCE OF 60-1441
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PROKAPYOTA: TENEFICULES:
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D: Mismatches
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Best Local &
Matches 5
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MEDLINE: 88036210.

RODRIGUEZ J.F., ESTEBAN M.;
J. VIROL. 61:3550-4554(1987).

-I. FUNCTION: THIS PROTEIN APPEARS TO PLAY AN IMPOPTANT HOLE IN VIPTE PENETRATION AT THE LEVEL OF CELL FUSION. THE N.TERMINAL PROXIMAL REGION IS ESSENTIAL FOR FUSION ABILITY. ESSENTIAL IN PUSING THE OUTERMOST OF THE TWO GOLGI-DERIVED MEMBRANES ENVEL FING THE VIPTE
                                                                                                                                                                                                    01-JUL-1989 (REL. 11, CREATED)
C1-WARK-1992 (REL. 21, MAST SEWDENCE UF
01-FER-1994 (REL. 28, MAST ANNOTATION
14 KD FUSION PROTEIN.
                                                                                                                                                                    VACCINIA VIRUS (STRAIN WR)
VIRIDAE: DS-DNA ENVELOGED V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VACCINIA VIRUS (STRAIN COPENHAGEN) VIRIDAE, DS-DNA ENVEL-PED VIRUSES.
                                                                               SEQUENCE FROM N.A.
                                                                                                   AMEGADZIE B.Y., AHN B. Y., MUSS B.;
J. BIOL. CHEM. 266:13712-13718(1991).
                                                                                                                         MEDLINE; 91310644.
                                                                                                                                      SEQUENCE FROM N.A.
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CARBOHYD 60 60
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VISCLUDY 179.247 266(1990)
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                                                                                                                                                                                                                                                                                                                   75 NDEVLF 80
                                                                                                                                                                                                                                                                                                                                      1 NDQVLF 6
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SUBCELLULAR INCATION: ENVELOPE FRACTION OF VIPTOMS
SIMILARITY: TO OTHER POXVIRUSES FUSION PROTEIN.
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5; Conserv
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LAST SEQUENCE
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Pred. No. 5.1:
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Best Local S
Matches 5
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EXTRACEPTINIAN CONVALENTLY LINKER

1. SUBCHIT. HONOTHINE CONVALENTLY LINKER

1. SUBCRITTON FOOTHER PROTITION OF VIPTONS.

1. SUBCRITTON TO OTHER POXVIPTSES FUSION PROTEIN

B. EMBL. M61187; G355629; -.

BEMBL. M51173; G355629; -.

BEMBL. X57318; G62244; ...

EMBL. X57318; G62244; ...

EMBL. X57318; G62244; ...

FIR. A07173; WMV114.

FIR. A07173; WMV114.

FIR. SIGNIE SIGNIE SOURCE SOURC
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Best Local
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SIRAINANE 95204215.
MEDITNE 95204215.
MANGER WANGEGIAYANGUN 5.
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948455;
91-NOV-1997 (REL. 35, CREATED)
01-NOV-1997 (REL. 35, LASI SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LASI ANNOTATION TREATE)
01-NOV-1997 (REL. 35, LASI ANNOTATION TREATE)
HYPOTHETICAL 44 & Kr. PROTEIN IN TPS FEATURE)
KLESSIELLA PREMMONIAE.
PROKABITITAL SEATILICUTES: SOUTHWATTERIA: FACULTATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. BACTERICL. 177:1788 1796(1995).
EMBL: D21111: G747668:
HYPCTHETICAL PROTEIN.
SECTEMON TOP 5A 44775 MW. AIN
                                                                                                                                                   CAENTSHABITITS ELEGANS
EDEARTITA METATIA, AC
                  STRAIN-BRISTOL N2.
PAULEY A.;
                                                                                      SECHENIE FROM N A
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98. 88
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Prod No 18
1 Mismatches
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Pred. No. 5.1:
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15_MOUSE STANDARD: PRT: 5
16.5020; O1-APR-1990 (REL. 14, CREATED)
10.40F-1990 (REL. 14, LAST SEQUENCE UP
10.0T-1996 (REL. 34, LAST ANNOTATION
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EMPO J. W:137-2050)v
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GENOMICS ***$41-$49(3940)
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--- STACE OF MEIOTIC PROFIBASE.
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                                                                                                                                                                                                                                                                interferon-g
feron-gamma i
                   interleukin
interleukin
                                  interleukin
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RESERVATE SOLUTION OF THE PROPERTY OF THE PROP
17-JAN-1995.
17-JAN-1995.
2 13-JUL-1995.
304906.
2 13-JUL-1995.
3P-045057.
3P-045057.
3P-045057.
4 (HAYB) HAYASHIBAR SEIBUTSU KAGAKU.

Kohno K, Kunikata T, Kurimoto M, Okamura H, Taniguchi M: Tanimoto T, Torigoe K;

Tanimoto T, Torigoe K;

Tanimoto T, Torigoe K;

Tanimoto T, Torigoe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIT FXCE-ID that induces games interferom grade in impresent profile used a g as antiviral or antitum-our agent, also induces FT Typick wirty of Kilker on 11s

FY Typick wirty of Kilker on 11s

FY Typick wirty of Kilker on 11s

FY Typick and Species of Figuresia if the Fritein if the invention for Geometry and Species represent fragments if the Fritain in the Invention for immunocompetent cells. The profess interfers and platein increasing agent.

GO antitument, antiseptic immunoregulatory and platein increasing agent.

Of the osa of the training of proposition and platein increasing agent.

Of the osa of the profess of the osa is to induce Iffgamma production in cultured cells. The profess was also be used to induce Iffgamma production in cultured cells and when used with interfeable (cilic) and temour of necrosis factor (INF), may improve the effect (or reduce side effects) of allowing immunotherapy in temours. The FNA envolute in the profess of allow as immunotherapy in temours. The FNA envolute in the profess of allowing a value of the produce the protein which yer then purified the sequence.

Sequence 18 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 6
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30.AUG 1996 (first entry)
30.AUG 1996 (first entry)
Interferon gamma production inducer peptide #2.
Interferon gamma inducer IFNgamma immunocompetent cell: antiviral: antitumour, antiseptic, immunoregulatory, platelet-increasing agent; therapy, presention, coulyloam a commination; repul concer, brain concer, granuloma: mycosis fungoides; rhoumatism; allorgy; cytotoxicity; AIDS: Killer Treel; interleuklic2, IC-2, tumour mechanis factor, TRF; adoptive immunotherapy, mornoclonal antibody.

Synthetic.
Ep-692536-A2.
                                                                      02-SEP-1996 (first entry)

O2-SEP-1996 (first entry)

Interferon gamma production inducer protein.

Interferon gamma, inducer, IFMyanna, inmunocomposted cell, antiviral;

antitumour; antiseptic; immunoregulatory; plateletrinoreasing agent;

therapy, prevention, dondyloma aduminatum, rend; dancer, brain dancer;

therapy, prevention, dondyloma aduminatum, rend; dancer, brain dancer;

therapy, prevention, dondyloma adumination, rend; dancer, brain dancer;

therapy myonsis functions, in 2, tumour necrosis factor, TMF;

adeptive immunotherapy; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                   R92506; standard; Protein; 157
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                                                                  Mus musculus.
isc_difference
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   Location, Qualifiers
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Higher interfers tamma inducer protein.
Calcular of the analysis protein; FRN quamma; antiviral; viruside; addition of the analysis of the approximation.
The approximation of the analysis of the approximation.
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In the seed to treating or proventing AIDS, condyloma acuminatum, read or the treating or proventing AIDS, condyloma acuminatum, read or the treating or proventing AIDS, condyloma acuminatum, read or the treating and my sais tungoides, recummation and invertey of the production in a contract with the IPNA many languages retroagly induces cytotexisity of Air or the selection of the production and with interleukin-2 (IL-2) and tunguage over the interleukin-2 (IL-2) and tunguage or the interleukin-2 (INF) may language the effect (or reduce side offects) of the IPNA may language. The DNA encoding this sequence can be presented by protein, which can then be purified (or assayed) as the model of the protein action, which can then be purified (or assayed).
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Fikile S. Febrer Kerbikata I, Ku
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Example B. I have the dample English. As the bound of a control of the region of a control of immuner operation colls is the product of a control of the colls. In the colls is the product of a control of the colls.
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Militaria 2007/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAYASHIBARA SEIBUISH KAGAKU
Mulikata I. Kurimoto M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that coduces gamma interferon producin immuno:competent used to as antivital or antitumour agent, also induces
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JP 58210.
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JP 5/2352.
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                                                                                                                                                                                                                                                                                                                                                       Re number rodn. inducing polypeptide - useful ear, with disease, malignancies and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Camumored Glator: adoptive immunotherapy;
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                                                                                      Query Match
Best Local Similarity
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Best Local Similarity
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15-NOV-1994: JP-304203.
23-FEB-1995: JF-028240.
10-MAR-1995: JP-078357.
18-SEP-1995: JP-262062.
29-SEP-1995: JP-274988.
                                                                                                                                                                           A novel human protein (89958) induces interfer or-damma (IFN-damma) prodon by immunocompetent cells to prodon set by induces the cytotoxicity of killer cells addyct induces the formation of killer cells (c.d. NK cells) lymphckine-activating killer (IAK) cells, and cytotoxic Treells). Recombinant IFK-damma inducer protein can be produced in high yields using host cells, esp. Escherichia cell, transformed with a vector carrying the encoding cDNA (T32402). It is useful as an antiviral antitumor, antibacterial, immunorceptiatory and blood platelet enhancing adent, and can be used in adoptive immunorhorapy It is also used to raise monoclonal antibodies. A full length sequence is given in K99560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR amplification of the CNNA (see also T32404-10) and expression in Escherichia coli XI-1 Blue MRF Kan allowed produce of recombinate inducer protein. This was used to construct hybridoma H-1, which produced anti IFN-gamma inducer protein manocional antibody H-1mAL useful in the detection and purification of the inducer pratein (see also R9958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1996 (first entry)
Human mature interferon-damma inducer protein.
Interferon-gamma inducer protein, IFN-gamma, autivital, virucide, antitumour, antibacterial, (mmunuregalatut, ad-etice (mmunothorapp)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R99558 standard; Protein; 157
R99558;
29-SEP-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WF:, 96 252837,25.
N-PSDB: T32402.
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Eukuda S. Kobno K. Kunikata T. Ku
                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 40; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        disorders
                                                                                                                                                                                                                                                                                                                                                                                                                        to treat and prevent, e.g. viral disease, malignancies and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding interferos-gamma prodm.-inducing polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Taniquehi M. Tanimoto T.
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30 FEDMID 35
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                                1 FEDMID 6
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                                                                         Conservative
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                                                                                      100.0%; Score 33; DB 1; Length: 157; 100.0%; Pred. No. 2.7;
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                                                                         Mismatches
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Best Local
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15-NOV.1994, JP -804209.

29-FFFF 10-40-17 p. 1904209.

10-MAR-1995, JP -078357.

18-SEP-1995, JP -278362.

29-SEP 1995, JP -274988.
                        22-MAY 1996.
10 NOV 1995. 3080005.
10 NOV 1995. 3080005.
10 NOV 1995. JF-208240.
10-XFF-1995. JF-208257.
18-XFF-1995. JF-208268.
20-XFF-1095. JF-208268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example A-2-2: Page 36-37, 48pp, English.

A novel mouse protein (F99559) induces interferon-gamma (IFN-gamma) produced by immunocompetent cells. Its sequence was deduced from that of a cUNA colone (13403) isolated from a mouse liver library Emomblement IFN-damma induces protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a vector assignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP-711
22 MAY
                                                                                                                                                                                                                                         Human interferon gamma inducer protein. IFN-gamma, antiviral: virucide, interferen-jamma inducer protein. IFN-gamma, antiviral: virucide, antiviran: antibecterial: immunorequiator: adoptive immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          carrying the cDNA. Sequence 157 AA.
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WPI; 96-252007/26
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10-MAR-1995 JP-078857
18-SEP 1995 JP-07866,
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The mature portion of a nevel bused protein (ABSE)) induces interferon gamma (IEM-gamma) produce by immunocompetent cells. It is the product of a cinA clone (ISA404) obtd. Itom a numun liver likrary. The profess containes the greatexistic of Eller cells and/or induces the fermation of the greatexistic (e.g. NE cells lymphokine activating killer (LAK) cells, and cytotoxic Tecels! Lymphokine activating killer (LAK) is useful as an antiviral ontitumer, antibacterial, immunocepulatory and blood plattlet calinoistic jace. Tel to be used in adoptive immunotherapy. It is also used to raise menoclonal antibodies.
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Example A.3-6; Page 17: 48pp; English.

Tryptic peptides (F9956) and F99562) correspond to amino acids 79:10 and 140; Respectively, of a novel interferon gamma (TENgamma) inducer protein identified in mouse liver. The Ferrish and the amplification of mouse liver CNNA, leading to utilised in the amplification of mouse liver cNNA, leading to the isolation of a number of a current of a current of the isolation of mouse liver cNNA.
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Sequence 18 AA
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Fukuda S. Kohno K. Kudikata I. Ku
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WEL: 96:528837/26.
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2011 Sociarity 100,0%, Prod. No. 2.7
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                                                       10-JUL-1997. U20432.
20-DEC-1996: U20432.
29-DEC-1995: US-580667.
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W31757:
15-JAN-1998 (first entry)
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This sequence represents a protein which induces interferon-damma probabilities in immunoscompetent reals. This protein may be used as production in immunoscompetent reals. This protein and treatment of the major component in a drug for the prevention and treatment of e.g. malignant tumcurs, wiral diseases, banterial hitcotions and
                               WPI; 97-363677/33.
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Interferon gamma inducing factor 1, IGIF-2, leaduryte, symphocytes huma
inflammation: proliferation: differentiation: majuration: tissue damage
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10-MAR-1995; JP-078357
29-SEP-1995; JP-274988
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compounds to diagnose, treat or prevent tissue dumage associated
              Novel interferon gamma inducing factor-2 - used to screen to:
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17-JUN-1997.
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PS Chaim is Pauce 46; 60pp; English.
PS Chaim is Pauce 46; 60pp; English.
PS Chaim is the protein sequence of interferon gamma inducing factor-2
CC (IGLP-2). An IGLP-2 warrant (W2775) and an IGLF variant (W22049).
CC Which may be an ulternate transcript, also exist. Probes derived from the nucleic acid sequences can be used to guantify the expression of CG IGLP-2 in conditions that are associated with inflammation or aberrant expression of IGLP 2. The protein can be used to screen for compounds that interact with IGLF 2, such as antibles, antagonists or other can hibitors (Specially Tibograpes or antisense sequences) of IGLP-2
CC expression of IGLP-1 industry. The protein can also be used to diagnose, provent of treat IGLP-2 industry. The protein can also be used to diagnose, provent of treat IGLP-2 industry, expecially in relation to tissue damage associated with inflammation.

So Sequence 193 Aa:
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W09724441-A1.
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Interferon gamma inducing factor 2 (IGIF-2, leading to factor) information; maturation; information; grollferation; differentiation; maturation;
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14-JAW-1998
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must by multiple; the IDIE'S sequence presented in Weince 193 AA;

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Inthitiatio gamma inducing factor:2 - used to screen for
ide to diagnose, treat or prevent tissue damage associated
                                    Similarity
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Similarity 100.0%; Prod. No. 3.4;
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FIS Disclosure, Page 22, 26cp, English

CC The present sequence represents a newel protein from mouse liver cells, which induces interferent squamma (IIN gamma) production in immunocompetent cells, and induces their formalism. It is used as an actionabile agent for antifumour cells and induces their formalism. It is used as an actionabile agent for antifumour immunotherapy, an antiviral (including anti-AIES) or antibecterial agent, and in the free treatment of attable of immuno system discourses, e.g. asthma, and in the treatment of attable of immunotherapy or asthma, it is also cased to treat leukepaenia and thrombocytopaenia associated with complete the indictionability improves the insultingual immunotherapy. This novel protein significantly improves the insultingual immunotherapy, this novel protein significantly improves the insultingual protein significantly improves the insultingual and other cancers. When there administered to the patient (before comministeration of II-2) or by addition to the patient (before compared for return to the patient) are being grown.
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                                                           Homo sapiens.
Er-767178-A1.
09-APR-1997.
  26-SEP-1996;
20-SEP-1996;
26-SEP-1995;
                                                                                                                   L6-JAN-1996 (first entry)
N-terminal fragment of interferon gamma inducer protein.
Interferon-gamma, INN-gamma, activital, anticomotic; radiother interferon-gamma, INN-gamma, activital, anticomotic; radiother immunosrepitatory, actit.miner agent, chem.therapy, leak-gammina thrombosytopeenia, theunounspetent cell; asthma; hayfever; rheumatism; interleukin; killer cell.
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Mouse Interfersa-gamma inducer protein.
Interferon-gamma, IPN-gamma; antiviral; antioncotic: radiotherapy:
Immunorequatory, antitument agent, chemocherapy, ic.k-paenia:
thromborytopaenia invole-competent cell: asthma: baytosor:
thromborytopaenia invole-competent cell: asthma: baytosor:
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20-SEP-1996; UP-269105,
26-SEP-1996; UP-270725,
29-FEB-1996; UP-2707244,
(PAYE ) HARASHIBAFA SELBUTSU KACAKU.
AKITA K. FUJII M. Kurimoto M. Nukada Y. Tanimoto T;
WPI; 97-205381/19.
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JF-270725.
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WE 1974 (ARTERIA ETHEROLE M. WHELLE Y. Tarimoto T

Human protect (colls useful for adoptive immuno, therapy of
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CC IL-2 alone, either when administered to the parient (before 22 administration of IL 2) or by addition to the addim in which colls of (intended for return to the patient) are being grown.

SO Sequence 157 AA:

Query Match
Best Local Similarity 100.0%: Score 33, DB 1: Length 157: Matches 6: Conservative 0: Mismatches 9: Indels 0: Guis Oy 1 FEDMTD 6

Db 30 FEDMTD 35

Search completed: Tune 22, 1999, 19:56:39

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OM protein : protein search, using sw model

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Title: US-09-030-061-2
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## SUMMARIES

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DNA, Res. A., F. 44, [19]
DNA, Res. A. (2) and the construction of the construction of thomosome 3p22:p21.3 that is
A. (3) to receive technology (5) 707
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de na la DD, repair profess (8ADA, profess verevisiae)
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(4-5) [7-0-814] A42842; Jeoget] 805779
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1: Mismatches
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~@smids 0229, 9115, 9192.
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A Experimental source strain $2880
e Garria Gartalon Blatter V
Yeast 10, 231 245, 1994
A:Title: The complete sequence of an
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A.Rosidaes: 1221/Y,224,77,226 754 .COU.
A.Griss references EXELMC4929 NID.;172334,
P.Glety, P.D.: Prakash, S.
Gene 74, 535-541, 1988
                                                                                                                                                                                                    A:Molecule type: DNA
A,Residues: 1 1071 <GAR>
A:Cross-references: EMBE:227116:
                                                                                                                                                                                                                                                                                                                   A; Status: translation not shown
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F;410-416/Fegion: basic
F;711-754/Region: acidic
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J. Bacteriol. 171, 1862-1869, 1989
A.Tille. Nucleofide seguence of the wild-type RAD4
A:Reference number: A32832, MUID.89197751
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A;Tressitofitesite (MM: 21971)
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A:Residues: 1-754 <MUL>
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Pred. No. 77;
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A.Experimental source, strain $2880 F.Brigose, S. Couto, J.R.: Guthrie, C. F.Brigose, S. Couto, J.R.: Guthrie, C. Cell 60, 705-717, 1990 Cell 60, 705-717, 1990 A.Title: A putative AIP binding protein influences the ride by of brancipolatics. A:Reference number: A32720: MUID.90162561
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R;Baladron, V., Ballesta, J.P.G., Bou, G., del Rey, F.; Esteban, P.F.;
submitted to the Protein Sequence Database, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding protein PRP16 - yeast (Saccharomycee cerevisian)
Nolitinate names: protein YKP086W: protein YKK406
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
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A;Crose-references: GP-M75959; NID:q172332; PID:q172333
C;Comment: This protein is one of the products of five genes assautial together
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A;Accession: JS0081
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A:Closs references: solutation1794; MIPS:YKRON6W
A:Map position: 11R
C.Sepenfamily are rived brakel box helicases; DEAL/H box helicase homology
C.Regwords: Arr SEAR box, hasheds: Floop, puring sucheotide binding
E:373-602,7 main SEAR box, hasheds: Floop, puring sucheotide binding
E:373-602,7 main SEAR box, hasheds in the Logy stealer
E:373-902, hashed box binding motif A (Piled)
E:463-91-7-7-8-10; bashed-binding motif B
E:473-476 /Positon DEAR motif
E:379, binding SEAR box Arr (Inc. as's' a gradious')
A-Ampression (1970)
A-Status: preliminary
A-Molecule type: DNA
A-Residucia: 1942 (200)
A-Cores references (MCT.MC202)
C-Keywords: fibronectin binding
                                                                                                                                                                                                                                                                                               fibromeetin/binding protein B - Staphylococcus aureus
0:Species: Staphylococcus aureus
0:Date: 13-7an-1995 #sequence_revision 13-7an-1995 #text_change 09-Sep-1997
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S19702
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A:Accession: $24378
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A:Status: translation not shown
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A:Cores::::(ormane: DMS: M6/604 NID 3458
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R:Alterachmid: " B Frie V Fachs G
Eur. J. Biochem. 207, 315-722, 1992
A:Title: Hovel harribin 2 auto because notabulism
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A:Moleculo typo: DNA
A:Mosibles (1950-197 600-1971 cpgs)
A:Gloss-teferences: GB:M31524; NID:g172259; ELD:g172270
C:Genetics:
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Bur, J. Blocker, 2020 [1641-1045, 1931]
F. Tille, J. Stiffent Grove Parell Filternettin kinding proteins in Staphylococous
Aspeferons on the Standard Mills 2021/1475
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C:Species: Pseudomonas sp.
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A.Rossidues: 1-1321 cMATE
A.Grassire[armoles EMRE 544598, NID gR71933, EID-d1068610- pip-gR71937
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A. Pus. June 1 4-4, 72 4-7 1777. PS. Lill 1721 - MAS:
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A. Pus. Teferences. EMBL.M17539. NID.q1724-89, Fib.q1/24-90
B. Nailes, M. Craws, M. Sasandra, S.L. Kikayazhli M. Hailanta, H. Shibata.
Yeast 11, 1525-1532, 1995
A. Little Sequencia of at 1818 &b fraymout from Eachiatomy, es cete/isiae chromo.
A. Reference number: 8604-95
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A.Title Veast mitochombrial FNA polymetare is bened good AlReference number A27336; MUID:88002333
A.Accession: A27336
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C:Accession: S37845; A55465: C55465
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A:Map position: 6L
A.Genome: nuclear
C:Keywords: mitochendrium, nucleatid;/transferase, transcription
                                                                                                                                                              R;Rieger, M.
submitted to the Frotein
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A:Residues: 1:1351 <MOR>
A:Cross-references: EMBI:D50517; NID-q845545; PiD-d1004443;
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A; Molecule type: 1
A; Residues: 1-482
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Titches 5: Conserv
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A.Status: mucleic acid sequence not shown: translation not shown
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H88929 N.C. H8862811 FLA. Sajra, N.H. Stickner, J.H.,
There for 1710 The late to Apply Section and hambledy to vertebrate protection.
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167-173, 1903
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Fred. No. 45:
Mismatches
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A:Experimental source: strain 168 C:Genetics:

NID. 32637 802,

issuperfamily: conserved hypothetical protein HIO365

C:Genetics:

yloN

A; Molecule type: DNA A; Residues: 1:363 < KUN>

A; Status: preliminary; nucleic acid sequence not shown; translation not

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Claccession: F69878

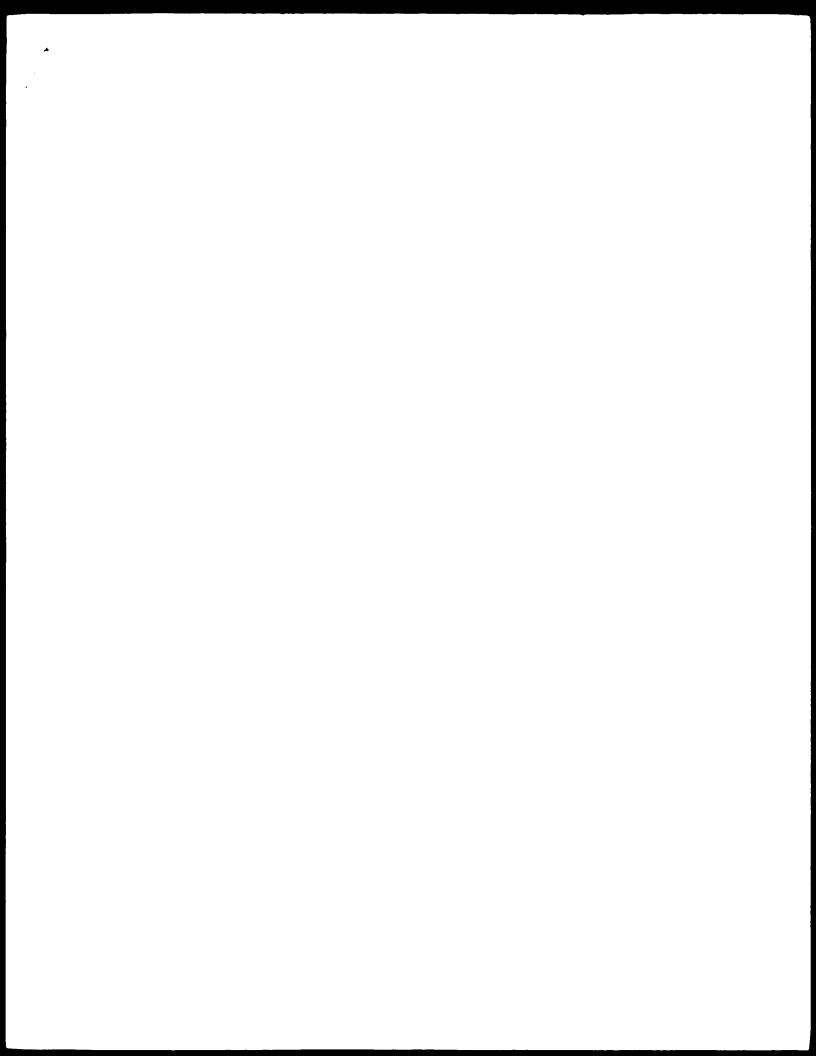
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R:Kunst. F. Ogasawara. N. Mcczer. I.: Albertini. A.M.: Alcuni. C.: Alcerdo. V.: Ber C.: Bron. S.: Brouillet, S.: Bruschi, C.V.: Caldwell. B.: Opinico, V.: Cultor. N.M.: A.: Brilch, S.D.; Emmerson, P.T.: Entian, K.D.: Errinaton, J.: Fabrot. V.: Forestil. Nature 90, 249-258, 1997

A:Authors: Fritz, C., Fujita, M., Fujita, Y.; Fuma, S.: Galizzi. A.: Galloren, N.: Ghwood, C.R.: Henaut, A.: Hilbert. H.; Holsappel, S.: Hosono, S.: Hullo, M.F.: Itaya. M. Koningstein G.: Kroph S.: Kumano, M.: Kurita, K.: Lapides, A.: Lardinois, S.: Manoel, M.: Kuntors: Lazarevic, V.: Lee, S.M.: Levine, A.: Lin, H.: Musuda, S.: Manoel, O.: Rocha, F.: Roche, B.: Park, S.H.: Parro, V.: Poll, T.M.: Portetolio, V.: Por Rivolta, G.: Rocha, F.: Roche, B.: Rose, M.: Sadaie, Y.: Sato, T.: Scanlos, E.: Schl Authors: Schropeter, R.: Scoffone, S.chiquchi, J.: Sckwaba, A.: Serot, S.: Schl Authors: Complete growth and Schlawa, H.: Danchin, A.

A:Title: The complete growth Soquence of the Gram-goville barterium Bacill.s shittill A: Reference number: A59880 MUID:98044033
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C:Species: Bacillus subtilis
C:Data: 05-Dec-1947 #sequence_revision 05-Dec-1947 #fext_clusto 24-Sep-1-+F
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A:Reference number: A70300: M010:9819556
A:Accession: H70342
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A;Residues: 1-410 <AQE>
A;Cross:references: CR:AECO0591: NID:g2992119; FID::L98/12/0; GD:AECO0657
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C:Species: Aquifex aeclicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 04-Sep-1998
C.Accession, E70342
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RESULT 15
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probable membrane protein WGL0750 · yeast (Sacchalomydes derevisiae)
N.A.ternate names: hypotherical protein G3219
C.Species: Saccharomydes derevisiae
C.Scession: S44022
R.Rieger, M.: Mueller-Auer, S.: Brueckner, M.; Schaefer, M.
submitted to the Frotein sequence Database, May 1996
A.Reference number: S64071
A.Reference number: S64071
A.Recession: S64082
A.Reference number: S64071
A.Residues: 1387 KRIES
A.Reference number: S44071
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C.Scenetics: transmembrane protein
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OM protein protein search, using sw model

Run on: Tune 22, 1999, 10.59 41 : Search time 45 16 Seconds (without alignments)

Title: US-09-030-061-2
Perfect score: 33
Sequence: 1 FEDMID 6
Scoring Fable Pinguico

Searched. 74019 segs, 26840295 residues

Database: SwissProt_36:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DAM: AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 2 KH
                                                                                                                                                                                                                                                                                                              7E03579
                                                                                                                                                                                                                                       PROTEIN_KINASE_ATP:
                                                                                                                                                                                                                 PROTEIN_KINASE_DOM
                                                         TAMARE FILE KENTERE KILL FERSEN RIE KERIMOTO MIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTIVITIONALES: NEMATIGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22135 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 43;
100.0%; Pred. No.
                                                                                                                                                                                       TRANSFERASE:
   3
                                                      PROTEIN KINASE.
ATP (BY SIMILARITY).
AIP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MET -> IS. (IN
                                Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FT -> IS. (IN REF. 4683D859 CRC32;
                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismathes
                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC DOMAINS OF SER/THE
                                                                                                                                                                                    SERINE/THREONINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECERNENTEA: KHARIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .4 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O'CALLAGHAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIER M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SHOWWHEEK F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COULSON A.,
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Query Match
Best Local Similarity
Tatches 5: Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
France 5: Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR16_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                         EMPL: M31524; G172270; -.
EMBL: Z2711b; G41590; -.
EMBL: Z25311; G486571; -.
PIK: S381b4; S38164;
F1K: S39127; S39127;
                                                                                                                                                                                      NP_BIND
MUTAGEN
SITE
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OI JUN-1934 (REL. 29) LASI SEQUENCE UPDATE)
OR JUN-1994 (REL. 29) LAST ANNOTATION UPDATE)
PRE-MRNA SPLICING FACTOR RNA HELICASE PRP16.
PRP15 OR YKROSSW OF YKY405.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                                                                                                                                                                                                                                                                                                                                                                                   SCHWER B., GUTHRIE G.;

NATURE 34944994 499(1911).

FINNITON: INLIENCES THE EIPELTY OF ERANCHPOINT RECOGNITION IN YEAST SPLICING. THIS IS RNA-DEPENDENT ATPASE WHICH IS ESSENTIAL FOR VIABILITY. IT MAY MEDIALE ONE OF HER MANY ALTO-RECOUNT HER RECOGNITION MAY BE COUPLED TO ALE BINDING AND/OF HYDROLYSIS.

THE SECTION OF THE STREET FOR THE SPLICEGOME.

THE SIMILARITY. TO OTHER "DEAD" BOX FAMILY HELICASES, BELONGS TO THE TEATH SUBFRAILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE: 94262327.

GARCIA-CANTALEJO J., BALADRON V., ESTEBAN P.F.. SANTOS M.A.,

REMACHA M.A., REVUELTA J.L., BALLESTA J.P.G., TMENEZ A., TE

YEAST 10.231 245(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 90182661.
BURGESS S., COUTO J.R..
CELL 60:705-717(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-APR-1990 (REL 14, CREATED)
01 JUN-1994 (REL 29, LASI SEQ
01-JUN-1994 (REL 29, LASI ANN
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                    MENA
                                                                                                                                                                                                                                                                  NUCLEAR PROTEIN
                                                                                                                                                                                                                                                                                                    FE. SIIL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
435 FEDVID 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       472 FDDMTD 477
                                  1 FEDMID 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 FEDMID 6
                                                                                                                                                                                                                                                                            L0001504; FKP16.
MIL. 1800090, CEAH_AIF_HECLOASE; 1.
FFOCESSING. MENA SPUICING, HECLOASE, AIR BUNDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91125476
                                                                                                                                                                  1071 AA:
                                                                        Conservative
                                                                                                                                                                                      373
386
473
698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                        380
386
476
                                                                                                                                                                                      869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.98;
83.3<del>8</del>;
                                                                                          87.9%;
83.3%;
                                                                                                                                                                  121652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 30: DB Pred. No. 43; 1: Mismatches
                                                                                                                                                                ATP (BY SIMILARITY).
Y->D: SUPPRESSOR PHENCIYEE.
DEAH BOX.
A -> R (IN REF. 1).
MW: E9FTOFEB CRC32:
                                                                    Score 29; DB 1;
Pred. No. 89;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1:
                                                                                                          Length 1071;
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RESULT 5
RAD4\_YEAST

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AVILES E. SERNO A. BPRINANT T. HENNESSEY K.M. ALLEN E. AFAUTO F.
RA AVILES E. SERNO A. BPRINANT T. CAPPENTER J. CHEEN E. CHERRY J.M.
RA CHUNC E. DYNDAN M. GUZMAN E. HAPTZELL G. HYNICKE-SMITH S..
RA HYMAN F. YAYSER A., KOMF G., LASHKAR D., LEW H., LIN D.
RA MOSEDALE E. NAKAHARA K., NAMATH A., NORGREN R., OFFNER P., OH G.,
RA PETEL F. K., ROBERTS D., SEHL P., SCHRAMM S., SHOGREN I., SMITH V.,
RA TAYLOR P. WEIT Y. YELTON M. HOTSTEIN D., DAVIS R W.;
RI CHORTON INVOLVED IN NOCLEGATION FROM SANKS.
C. TUNCTION. INVOLVED IN NOCLEGATION FROM FROM GASENTS.
C. TUNCTION. ROLLY TO EMPLICATE EXCISION FROM FAMAMALIAN XPCC.
REMEL MOSECLLULAR LOCATION: NUCLEBR.
C. TO SUBCELLULAR LOCATION: NUCLEBR.
C. TO SUBCELLULAR LOCATION: NUCLEBR.
REMEL MOSECON (170373) - .
REMEL MOSECON (170373) 
                              RESCUENCE OF THE SESSE OF THE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM MEANS

PROMITEAST STANLARD.

1 P13432;

1 C1-LAN-1950 (REL. 13, CREATED)

T C1-LAN-1960 (REL. 13, CREATED)

T C1-LAN-1960 (REL. 13, LAST SELHENTE HERATE)

OT O1-NOW-1965 (REL. 32, LAST SANMOTATION UPDATE)

BE DNA-DIFFTED WAS POLYMERASE MITOCHONDRIAL P

ON RPC41 OR TEL036M.

RPC41 OR TEL036M.

SACCHARDMYCTS OPPEVIOLE TRAKER'S TENASCOMY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SECTENCE FROM NIA:
STRAIN STORY AND THE AVITY OF THE AVIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAD4_YEAST STANDARD,
P14736;
O1-APR-1990 (REL. 14, CRE
O1-APR-1990 (REL. 14, LAS
O1-OTT-1996 (PEL. 14, LAS
O1-OTT-1996 (PEL. 34, LAS
DNA REPARA PROTEIN RAD4,
PAD4 OP YEP1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA REPAIR:
DNA_BIND
CONFLICT
SECTENCE 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A. MOILITAN TO DIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDITAR: PRAKASE S
GIBIZ R.D., PRAKASE S
GENE 74.500 S41(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                              YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SACCHAROMYCES CEREVISIAE (BAKER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBMITTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE: 89197751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDITAT: PARRIET PARRIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mutci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEDMID 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAYION O CHETETON E S .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1058: RAD4.
R: CNA-BINDING: NUCLEAR PROTEIN.
259 POTENTIAL.
259 VCI -> EGL (
223 225 VCI -> EGL (
754 AA: 87174 MW; BE65DEF2 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EEB-1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRIEDBERG E.C.,
L. 171:1862-1869(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.93;
83.33.
                                                                                                                                                CREATED)
LAST SELVENCE MEDATE)
LAST ANNOTATION UPDATE)
YMEPASE MITOCHONDETAL PRECUESOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO EMBL/CENPANK/CODET DATA BANKS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 29: DB
Fred: No. 61;
1 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
VCI -> EGL (IN R)
: EE65DEF2 CEC32
                                                                 HEMIASCOMYDETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
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|-1
|-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO MAMMALIAN XPCC
                                                                                                                                                                                        (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
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                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                   CEA_YEAST
D T2EA_YEAST
                                                                                                                                                                                                                                                                                                                                                  Substituted Similarity 83.
Matches 5: Conservative
RIBGER M.)
STERMITTED (MASSIZEA) 17 3
-1 FURNITION RESPONTES THE PNA POLYMERASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDULINE; 88002333.
MASTERS B.S. STOHL L.L., (
CELL 51:89-99(1987).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDILAR, S. MAITOU M. BALANCE MUFRARANT Y. NOLAN.

SASANIMA S.-I., SASANIMA M. ISSUCHIVA Y., NOLAN.

SASANIMA S.-I., SASANIMA M. ISSUCHIVA Y., NOLAN.

SASANIMA S.-I., SASANIMA M. ISSUCHIVA Y., NOLANE SASE CATALYZES THE TEANSCRIETION

OF THAT THE TIME FINAL THE EARL PROPRIETIS TRIPHOSPHATE = N. PYROPHOSPHATE -
                                                                                                                                                                                                                                                                                                                                                                                                                  GEAIN
ACT_SITE
ACT_SITE
ACT_SITE
CONFILCT
CONFILCT
                                                                                                                                                         OI-JUN-1994 (REL. 29, CREATED)
OI-JUN-1994 (REL. 29, LASI SEQUENCE OPDATE)
OI-JUN-1996 (REL. 34, LASI ANNOTATION UPDATE)
TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT (IFILE-ALPHA)
(IFANSCRIPTION EATOR A LARGE SCHONIT) (FACTOR A 56 KD SCHONIT).
TFAL OR YKLO28W.
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
                                                                       MEDLINE: 95050500.

FEAVER W.J., HENRY N.L., BOSHNELL D.Z FEAVER W.J., KORNERERG R.D.:

J. EIGE. CHEM. JEG: 27547-27553(1994).
                                                                                                                                                                                                                                                                                                          1300 FEDIID 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M17539; G172490; -
EMBL; M50r17; C1004843;
EMBL; E44599; G871977;
P19; A27736; A27336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE) PS00489; RNA_POT_PHAGE_2; 1.
PROSITE, PS00900; RNA_FOT_FHAGE_1; 1.
CNA-CIFETTET FNA FOTEMPRASE; TRANSORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                  STRAIN-BJ926
                                                    SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE PROM N A
                                                                                                                                                  EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPANSIT
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SUMMEDITAL DESALTON: MITOCHONERIAL SIMILARITY: RELONGS TO THE PHASE AN
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-5289C / AD972;
-2 9540532.
AMI Y 9540532.
AMI Y -1 , SASANIWA M TSTCHIYA Y
-7150 H., EKI I.;
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                                                                                                                              SECUENCE
                                                                                             BUSHNELL D.A.,
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1: Mismatches (
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BY SIMILARITY.
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SS -7 MF (IN REF. D).
MW: 40DLG84U GRGJJ:
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                                                                                              SAYRE M.H.,
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\frac{1}{2} FFEEET \frac{1}{2}
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Segri : 341
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TIN-103 (BELL 29 TREATE)

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TT-1 04 (RECO), CREALED
TT-1 04 (RECO), LAST SEQUENCE UPDATE;
TH 04 (RECOARMOXYKINASE (GTP) (RC 4.1.1.32)
H. JEHON N. PYPTVALE CARBOXYKINASE) (PEPCK).
                                                                                                    SOBITO CIMI
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**CLART STORMIT M. MENCEAR (PENBARLE).
**LARTY STROME, TO MAMMALIAN TEITE-ALPHA.
**LARTY STORMIT M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THAT THE TOTAL AND THE PROPERTY OF THE T
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WE STEELS:
WE WITHOUT AND THE STATE WE RESIDE TO THE THE STATE OF T
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ACTOS SES 265621 6629(1992)
IN TAY SAN TELLMENT THAN SQUIENCES.
CLULAR DEALTON: NUCLEAR (PROBABLE)
TARTLY BELLMES IN THE TELLMERE-BINDING
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                                                          GRATTLE THIES:
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                                                          ANOXYPHOTOBACTERIA: GREEN BACTERIA:
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Prad. No. 46;
C: Mismatches
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Fred. No. 38:
D: Mismatches
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78AB7561 FRC32:
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Best Local Similarity 83.3
Matches 5: Conservative
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 5: Conser
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RIFGER M. RPTFCKNER M., SCHAEFER M., YEAST 13.1077-1090(1997).

EMBL: Z72597; E243961; -.

HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
TRANSMEM 311 327 POTENTIAL
TRANSMEM 311 327 POTENTIAL
SECULENCE 387 AA, 44585 MW; HOF8386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YGH5_YEAST
P53159;
01-OCT-1996
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ACT_SITE
SEQUENCE
                                                                                         15-JUL-1998 (PRI. 36, CWRATED)
15-JUL-1998 (PRI. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (PRI. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (PRI. 46, LAST ANNOTATION UPDATE)
                                                                                                                                                 YLON_BACSU
034617:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (REL. 34, CREATED)
01-OCT-1996 (REL. 54, LASI SEQUENCE UPDATE)
01-NOV-1997 (REL. 55, LASI ANNOTATION UPDATE)
HYPOTHETICAL 44.6 KD PROTEIN IN RPL6-HSF1 INTERGENTARED HEROTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
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MEDLINE: 93192317.

MIE E.I., ITIL H. BAUSEA S., MAELA M., IJIA, M., IBIOCHIM, BIOPHYS. ACTA 1172:1267-273(1993).

-!- CATALYTIC ACTIVITY: GIP + GXALGACETAIE = GOP -
            STRAIN-168;
                           SEQUENCE FROM N.
                                                   BACILLUS SUBTILIS: PROKARYOTA; FIRMICUTES:
                                                                                 NOTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     + CO(2).
-!- FATHWAY: WAIE-LIMITING GLOCOMEGGENIC ENZYME.
-!- SIMILARITY: BELONGS TO THE PHOSPHOLEGLEVE TVAIL TARROTAYKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00505; PEPCK_GTP; 1.
                                                                                                                                                                                                                                 361 FEDQTD 366
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                                                                                                                                                                                                                                                          1 FEDMID 6
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IND 248 255 GTP (POTENTIAL).
SITE 299 299 BY SIMILARITY.
ENCE 646 AA: 72531 MW; 45D273AH CRC32
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U.,
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5 646 AA:
  ERRINGTON
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83.3%:
                                                      ENDOSPORE-FORMING
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                                                                                                                                                                                                                                                                                    Score 28: DB
Pred. No. 50:
0: Mismatches
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                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
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                                                                                                                                                              363 AA
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                                                                                                                                                                                                                                                                                              DB 1: Length 487;
50;
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                                                   AND COCCE BACILLAGEAR
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RESULT 12
CCH1_YEAST
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Best [moda] 9
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P50977:
                                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                     TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE, 98-01560.

PAIDHUNAI M. DARRET S.,
NOL CELL BIOL 17:6339-6347(1997).

-!! SUBGELIULAR 10:6ATTON INTEGRAL MEMBRANE FROTEIN (POTENTIAL)
-!! SUBGELIULAR 10:6ATTON INTEGRAL MEMBRANE FROTEIN (POTENTIAL)
-!! SUBGELIULAR 10:6ATTON INTEGRAL MEMBRANE PAID DALCIUM CHANNELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-S2801
MEDLINE, 97438481.
RIEGER M. RHIFCKNER M. «
YEAST 13:1077-1090(1997).
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TRANSMEM
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MEDLINE; 9526
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CCHI OR YGRZITW OR GB501, BAKER'S
SACCHARCMYCES CEREVISIAE (BAKER'S
EUKARYOTA, FUNGI, ASCONYCOTIUM, HE
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01-00T-1996 (REL.
01-NOV-1997 (REC.
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12:385-390(1996).
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ADDITITION F.S., MULICAN J.T., HENNESSEY K.M., ALIEN E., AFAUJO R.,

ADDITITION F.S., MULICAN J.T., CARPENTER J., CHEN E., CHERRY J.M.

AND CHEN F. RAYSER A., ROMP C., LASHKARI D., LEW H., LIN D.,

AND CHEN F. RAYSER A., ROMP C., LASHKARI D., LEW H., LIN D.,

AN OSFIALF D., NAKAHARA K., NAMATH A., NOPEREN R., OFFICE P., OH C.,

RA MUSEFALF D., NAKAHARA K., NAMATH A., NOPEREN R., SHOGREN I., SKITH V.,

RA PETEL F.X., POBERIS J., SEHL P., SCHRAMM S., SHOGREN I., SKITH V.,

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Best Local Similarity
Matches 5: Conser
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Post cocal Similarity 80.38,
Natches 5, conservative
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EMBL: $69371; G546371; -

EMBL: $69371; G546371; -

EMBL: 916916; 36.1375; -

PIR: $44446; $44446.

$500: L0000699; SDI1.
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O1 FER-1995 (REL. 31. CREATED)
O1-FER-1995 (REL. 31. LAST SECHENCE UPDATE)
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SECHETORY PATHWAY FOR PATSOCIATION INHIBITOR.
GELL OR SEC19 OR VERB1364. (BAKER'S YEAST).
SACCHAROMYCES CEPEVISIAE (BAKER'S YEAST).
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EMBO J. 13:1718-1728(1994)
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MEDLIND: 94208542.
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Prod. No. 97;
O: Mismatches
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Fred. No. 4.8e-CD
6, Mishatches
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AFAUJO R., CHERRY J.M.,

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15 (BEC 4 TASE SEGRENCE HEDALE)
15 (BEC 46 LASE SEGRENCE HEDALE)
18 (BEC 46 LASE ANNOTATION TEPDATE)
18 (BESTEWER 4 TESTES (BECTOR) (INTERFERON GAMMA INDUCING FACTOR)
18 (BEN JAMMA) (ROTTINE FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
18 A PARINT
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FIKABUNTA METAT AT ANNED MATES NEMATODA: SECERNENTEAT RHABDITIDA
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***NCT N. BERNSHALE POR THE DEACHTYLATION OF LYSINE RESIDUES ON BEEN TRAINED DATE OF THE CORE HISTORIES (H2A, H2B, H3 AND H4).

***STECT OF A TYLATION FLATS AN IMPORTANT ROLL IN IRANSCRIPTIONAL BESULLOID. N. HELLY ARRESSION AND DEVELOPMENTAL EVENTS (BY CMILIONIC).
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MURITARIH M.P.;

O THE LOOP TO FMALATENBANAZERA CALA FANES.

O N. AUGMENIS NATURAL KILLER CELL ATTIVITY IN SPLEEN CELLS

MULATUS INTERFERON GAMMA PRODUCTION IN THELPER TYPE :

S. SY JULIANITY)

B. C. LUZER (4)
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PET R. LAST ANNETATION SPEATE)
CONF. SEATELYASE OS (AS). ()
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Prod. No. 32:
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Title: US-09-030-061-3
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## RESULT 1 ILIB\_HUMAN SIANDARD; PRT; 193 AA. ID ILIB\_HUMAN SIANDARD; PRT; 193 AA. AC Q14116; ET 15-JUL-1998 (REL 35 GREATED) ET 15-JUL-1998 (REL 35 GREATED) ET 15-JUL-1998 (REL 35 LAST SECTION UPDATE) ET 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) ET 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) ET 15-JUL-1998 (REL 36 LAST ANNOTATION UPDATE) ET (INTERLEUKIN-18 PRECIPESOF (IT-18) (INTERLEUKIN-1 GAMMA) (II-15 GAMMA). 긷 Swery Match 190.0% Score 33, DB 1, Bost Local Similarity 100.0% Pred. No. 0.8; Matches 7, Conservative 0, Mishatches 0 SEQUENCE FROM N A AND TISSUE=LIVER; MEDLINE: 96061009. OFAMPIFA H TENTET H F TANIMITE T TITETTOF H SECTENCE EMBI, 049950, 31405319; -. EMBI, 090434, 31899240; -. MIM; 600953; -. TISSUE-PERIPHERAL BLOOD: O'NITH H. FIM S. J. HINLEL, CHUN H.S., Joh T.H.; SURMITHAL (FEK-1997) TO EMEL/SENBANK, DDBJ DATA BANKS. SURMITHAL (FEK-1997) TO EMEL/SENBANK, DDBJ DATA BANKS. \*\*\* FUNCTION ACCMENTS NATURAL MILLER COLL ACTIVITY IN SPLEEN COLLS AND SIMULATES INTERFERON GAMMA PRODUCTION IN THELTER TYPE I MEDLINE, VEC47646. DSHTO S. NAMBA M. OKTPA T. HATTOPI K., NUKADA Y. TANARP P. KONISHI F. MICALLEF M., FUTII M., TORIO FUKUDA S. IKEDA M. OKAMUBA H., KUBIMOTO M.) BOMO SAPIERS (HOMAN). EUKAFYOTA, METAZCA, CHCELATA, VERTEBEATA, TETEAPCCA, MAMMALIA: EUTHERIA: PRIMATES. IL18 OR IGIE. MUS MUZIMULE (MUGEL). EURARVOTA, METADOA, MEGROTAL VERTERRATA, TETENHOTAL YANMALIA! EUTHERIA: RODENTIA. PROPER CYTOKINE SEQUENCE OF 2-193 FROM N.A. SEQUENCE FROM N.A. IL18 OR IGIF. TISSUE=LIVER; 170 FELTLER 176 1 PKLILKK 7 IMMUNOL. 156:4274-4279(1996). CELLS 10 N 1.1 O 7 SET . α (.1 α (... α 3 ANT () #> 11.57.5 PUMATSU T., YUTSUDO M., PARTIAL SEÇÜENCE. × YUAK\_BAUSU E124\_METJA INTERLECKIN-18. TEESETIT CECS: BY SIMILARITY ALIGNMENTS ADA Y , AKITA K TORISOF K., TA HAKURA A., Echath 193: Hidele 945914 pactilus su 957588 methanocoed TANIMOTO T.. 0;

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01-NOV-1997
-:- SIMILARITY: TO YEAST BUD3.
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
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HYPOTHETICAL 43.6 KL PROTEIN.
DEFRARYOMYCES OCCIDENTALIS (YEAST) (SCHWANNIOMYCES OCCIDENTALIS).
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MEDLINE: 95321019.
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EMBL; AE000017; G1673817;
PROSITE: PS01008; DNAA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF CHROMOSOMAL FREI TATION RINGS TO THE DATA HER CONTION AND RESULATION OF CHROMOSOMAL FREI TATION RINGS TO THE DATA AT A 9 HP CONNENSUS IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 HP CONNENSUS (FINAL MAY), 5' ITAIC(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J,A)A(J
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Query Match Best Local Similarity

90.9**%**;

Score 30; Fred. No.

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COCCEPAX REPRESENTATION OF REP
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P21421: P21421 (PEL 1

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AROUTE P., MOSPE P.W. I.
STRATH M. J. GOLDMAN N. BARNETT P., MOSPE P.W. I.
STRATH M. J. MIYTE A., WILLIAMSON D.H., WILSON R.J.M.
MOC. BIOCHEM. FABASITOL. 60.111 [2] (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANN/TATION TERRATE)
INTERLEUKIN-18 PRECUPSOP (IL-18) (INTEPFERON-GAMMA INDUCING FACTOR)
(IEM GAMMA INDUTING FACTOR) (INTERFEUKIN-1 GAMMA) (IL-1 GAMMA)
ILD8 OR IGIF.
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F61928
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01-NOV-1997 (REL. 35, LAST ANNOTATION HPTATE)
DNA-DIRECTED RNA POLYMPRASE BETA CHAIN (EC. 2.7
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CONTI B., JAHNS J.
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                                                                                                                       SEQUENCE OF 328-1024 FROM N.A. MEDIINE: 91187055.
                                                                                                                                                                                                                                                                                                    STRAIN-BW
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EUTHERIA: RODENTIA.
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FUNGITON, AGGMENTS NATURAL KILLER OBLI ACTIVITY IN SPLEEN OBLIS
AND STINGLATES INTERFERENT GAMMA PRODUCTION IN T HELPER TYPE I
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                       ONER M.T. WILLIAMSON D.H. WILSON B.J.M.
BEOGREM, DAKASITOL, 44:115-124(1991)
BUNDILLE, LOAK-DEFUNDERU BEA FOLUMERASE CATALYZES THE TEANSCHIETION
STORM LATTERA HELDE FOUR KIBONGILEDSIDE TEIPHOSPHAIES AS
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35. LAST ANNOTATION
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2: Mismotobes
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MISSING (IN ISOFORM ALPHA).
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-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CI
EMBL; X7544, G58764; -.
EMBL; X7577; G9880; -.
EMBL; X5217; G9880; -.
EMBL; X95275; E220243; -.
EMBL; X95275; E220243; -.
PROSITE: PS01166; RNA_POL_BETA; 1.
TPANSCRIPTION; DNA-DIRECTED RNA POLYMERASE.
SECTEMBER 1044 AA: 122195 MW; S9EARFREI CRC32;
                                                                                                                                                                                                                                    -! CATALYTIC ACTIVITY, AIF L-LEUCINE - TANA(LEU) - AMP -
PROPHOSPHAIE + L-LEUCYL-TRNA(LEU).
-! SYMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
BMBL: Z35238; G1057059; --
EMBL: Z46787; G1057059; --
EMBL: Z46787; G1057059; --
WOPMSEU: P841; CE15217;
AMINOACYL-TRNA SYNTHIASE): FRIBLIS BIOSYNTHESIS, LIGASE; AIF BINDING SIMILAR
50 60 "HIGH" REGION.
SIMILAR 700 701 "PXSYS" PEGION.
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01-001-1996 (REL. 34, CREATED)
01-001-1996 (REL. 34, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
FRODADEL LEUCYL-16NA SYNIBLIASE (EC 0.1.1.4) (LEUCINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAEEL
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STRAIN-BRISTOL N2;
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ETEAFTITA, METALUA, ACCELUMNIES
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                                                                                                                                                                                                                                                                                                                                                                                                        SECCENCE
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    CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHUSEHATE

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Labibo MW: 74866501 CR032:
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Pred. No. 43;
C: Mismatches
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1. Mismatches
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AFILE HELDON'S I- PEPTIDASE FAMILY M20A; ALSO KNOWN AS THE CAPEZA YLZIFEZZYS'S FAMILY.
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(BELLAS, LASE SECUENTE OPDATE)

(BELLAS, LASE ANNOTATION OPDATE)

(BELLAS, LASE ANNOTATION OPDATE)

MACRO MODIFICITION OF ANY MODEL OF A LEHTCEOGUL MATE SPECTHASE

MACRO MODIFICATE DEHYDRATASE (EC. 4.2.1.10)

MODIFICATION SHIRIMALES DEHYDRATASE (EC. 4.2.1.10)

MODIFICATION SHIRIMALES DEHYDRATASE (EC. 2.5.1.19)).
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1. A TIVITY - FIRSTHORADE POLYAROMATIC AMINO ACID BIOSYNTHESIS.

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2001-00 ARGE_DAFE_CPG2_1; 1.
ACTOMISSING HYDROLASE; METALLOPBOTEASE
                                                                                                                                                                                                                                                                                                    CHOSE DEHYDROUDINASE_I; ].
CLI = SHIKIMAIE_KINASE; ].
CLI = CLI = CONTHENSIS, METHEORETICNA; ENERME
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* DEHYDROQUINASE.
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01-FEB-1995 (REL. 31
15-JUL-1998 (KEL. 36
PEPTIDE SYNTHETASE 2
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ACT_SITE
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                      GRANDI G.;
MICHOBIOLOGY 141:645-648(1995)
-!- COFACTOR: CONTAINS A COVAL
                                                                                                                                                                                                            BACILLUS SUBTILIS. PROKARYOTA: FIRMIO
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1 SIMILARITY BELLONGS TO THE CYTOCHROME P45 FAM
EMEL, 124128, 5102944;

PROSTITE PSONORA CYTOCHROME P450; 1.

OXIDARFUNCTASE ELECTION ISANSPORT: HEME.
METAL 436 436 HEME (BY SIMILARITY).
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01-FEB-1996 (REL. 33, LASI SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LASI ANOTATION UPDAT
CYTOCHROME P450 LXXIB1 (EC 1.14.14.+).
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                                                                                                                                                                                                                                                             PPSB OR PPS2.
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                                                                                                                 MELLINE,
                                                                                                                                         STRAIN-168
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                                                                                                                                                               SECUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EUKARYOTA; PLANTA: EMBRYOPHYTA; ANGLOSPERMAE; DICCIYLEDONEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYP71B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UDVARDI M.K., METZGER J.D., KRISHNAPILLAI V., SEAC YE W. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                        COMONI A., FRANCHI E., MAGISIRELLI
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1581 AA; 178043 MW; B914BECC CRC'2;
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                      CONTAINS A COVALENTLY BOUND PHOSPHOPANTETHEINF
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31, LAST SEQUENCE UPDATE)
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Pred. No. 31;
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Fred. No. 98:
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SULTREES 1995 (REL. 33, LAST AN
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PROSITE: PS00455; AMP_BINDING; 2.
PROSITE: PS50075: AGP_DDMAIN: 2.
MULTIFUNCTIONAL ENZYMF: LIGASE: PEPEAT;
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EMBL: Z99113; E1183491;
SUBTILIST; BG10971; PPS;
            NUCLEAR PROTEIN
                            FIR, A40711, A40711.
TRANSFAC; T02148; -.
SGD: L0002051; SRB4.
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MEDLINE: 93
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TROMPSTW T M . KTIESKE A
CELL 73:1361-1375(1993).
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L: L12JU5: G172693: -.
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U1: EEC:1932 (REL. 24, CREATEU)

O1: DEC:1992 (REL. 24, LAST SEGUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

TPANSCPIDITION INTIACTION FACTOR IIB (TFIIB).
                                                                               REPEAT
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HOMO SAPIENS (HUMAN).
EUKARYOTA, METASCA, CHO
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NATURE 352:689-695(1991)
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PDB; 1TFB; 12-MAR-97.
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MALIK S., HISATAKF K
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(IGIF 2) An IGIF 2 variant (W21757) and an IGIF variant (W21049), which may be an iterate transcript, also easier Produce derived from the novoleto acid sequences can be used to quantify the expression of IGIF 2 to conditions that are associated with inflammation or aberrant expression of IGIF 2. The protein can be used to stroke for corporate that interact with IGIF 2. Such as antibodies, antagonists or other inhibitors (especially ribotymes or antibodies, antagonists or other expression or activity. The protein can also be used to diagnoze, proven inhibitors (especially ribotymes or antisease expleness) of IGIF 3 expression or activity. The protein can also be used to diagnoze, proven it is that inflammation.

(Figure 193 AA)
                                                                                                  W46592:
21-MAY 1398 (first entry)
Amino acid sequence of human interleukin-1-gamma.
Interleukin-1-gamma, It-1-gamma, mouse, cytokine; IGIF, interleton-gamma; induction artifody dianosett assay, fusion protein, activity; immunological disorder; allergy.
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Cocks BG, Coloman R, B
WFI; 97-363577/33.
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20-EEC-1996: U20422.
29-DEC-1995: US-580667
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14-JAN-1998 (first entry)
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Therform gamma inducing factor:2, IGIF:2, levelsyte: lymphocyte;
inflammation, proliferation, differentiation; maturation, tissue damage:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W22047 standard; Protein: 193
                                                                    Homo sapiens.
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Location/Qualifiers 41. .47
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100.0%; Pred. No. 6.2e-83;
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                                                                                                                                                                                                                     SVK YEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * I boman interlegkin-1 gamma - used for treating
cold disorders caused by Haman II legamma
in bases 44-55; (Appl. English.
Classication represents biman interlegible-1-gamma) (II-1-gamma)
cols for luman equivalent of a mouse cytokine, IGIF, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burlens TT. Kastelein RA, Saba TR, Timans JC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     resed by human II. Fadamma protein can be covalently a crossed by human II. Fadamma protein can be covalently to a dynamical composition for supplying the full composition for supplying the full composition for supplying the covalent of the functional composition for supplying the covalent of the functional composition for supplying the covalent of the functional conditions that can be treated using the functional function include immunological disorders, allegates us its eases. The II. I damma can also be used to detect the
                                                                                                                                                                                                                                                                                                                                                                                                                          the protoin or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 wells to produce interferon-gamma. Human T
how 71% identity at the nucleotide level and
                                                                                                                                                                                                   * identity at the amino acid level.
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                                                                                                                                                                                   THE TENETH SEEDINGS IN THE STATE OF STREET OF STREET
                                                                                                                                 GERGELANDERSEMETVONED 157
                                                                                                                                                                                                                                                                                                                                      100.0%; Score 816; DB 1; 100.0%; Pred. No. 5.20-83;
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Human interleukin 18

16-NOV-1998 (first entry)

W77077 standard, peptide, 157

02-SEP-1998. 24-FEB-1998; 301352

Homo sapiens. EP-861663-A2.

Human; interleukin-18; IL-18; osteoclast; hypercalcaemia; osteoponia; osteoclastoma Behcet's syndrome; osteosarcoma; arthropathy; osteoporosis; chronic rheumatoid arthritis, deformity ostitis, primary hyperthyroidism.

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Best Tocal Similarity
Matches 197, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                     immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGIFs are also claimed to be useful for treation hepatitis, acquired immunodeficiency syndrome (AIDS), malaria, thereviosis, solid malignant tumbous (e.g. renal carcinoma), rheumatism, osteoporosis and thrombepenia caused by radiation—and chemo-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of stimulating immunocompetent cells for the production of interferon gamma and are chaimed to be less toole, more active and stable than the corresponding will type IGIF The movement IGIFs are also claimed to enhance killer cell cytoroxicity and/or induce killer cell formation, and may therefore be useful as antitumour agents, antitumour agents, antitumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antitumour, antiviral, antimicrobial or anti-immunopathic agents
Claim 3: pages 36-37: 59pp: English.
The present sequence represents the wild-type imman interferon-damma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           induction factor (IRTE) the invention provides for mutant human and mouse interferon-gamma inducing factors in which one or more cystolog residues are replaced with different residues at a way from the consensus sequences shown in W48956-W48958. The mutant IGIEs are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-845530-A2.
03-JUN-1998.
28-NOV-1997; 309632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutants of interforon-gamma inducing polypeptide - useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents
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N-PSDB; V32754
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29 NOV-1996; JP-333037.
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144 EGYELACEKERULEKLILKKEHELGURSINEIVONEU 180
                                                 101 BOYELATEKPER ESELLEKSELDESE SIMETVENED 157
                                                                                                                                          61 AVTISVKCEKISTLSCENKIISFKEMNPPDNIKDTKSDIIFFGRSVPGHDNKMCFESSSY 120
                                                                                                                                                                                         74 YFGKLESKLSVIFNLNDQVLFIDQGNEFLFEDMTDSDCRDNAF-kT:F1:SMYKUSQPRGM + 3
                                                                                                                                                                                                                                     1 YEGKLESKLSVIRNINDOVLFIDOGNAPIFEDMIDSDORDNAPRITE1ISMYKDSOFRGM 6
                                                                                           AVTISVKÇEKISTI SÇENKI ISEKEMNEPENIKETESETIFEÇESVEÇIL MEMÇEESSSY
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                                                                                                                                                                                                                                                                                       Conservative
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Best Local
                                                                                                                                                                 THAYE : HAYASHTBARA SEIGHTSU KAGAKU
Gillespie MT. Horwood NJ, Kurimoto M, Udagawa N;
WPI: 98-448964/39.
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                                                       Thibition of estendiast formation. This is used for treating of preventing estendiast related diseases e.g. hypercalcaemia, estendiastoma Behenria modifical assessions arthropily objective thought if arthropily the defending and arthritis, deformity estitis, primary hyperthyroidism, esteopenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interlettin 18 active profess and precursor.
Interlettin 18 active profess and precursor.
Human: interleukin-18: IL-18: osteoclast; hypercalcaemia; osteopenia;
osteoclastima Boloet's syndhome, usteosarocma, arthropathy, osteoporosis,
osteoclastima Boloet's syndhome, usteosarocma, arthropathy, osteoporosis,
osteoclastima boloet's syndhome; usteosarocma, arthropathy, osteolasmi
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02-SEP-1908.
04-FEB-1908. B01361.
25-FEB-1997: JP-055468.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W77082 standard. Protein: 193
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ses 157: Conser
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                                                                                                                                                                                                                                                                                                                                        interleukin-18 to inhibit osteoclast formation - in treatment
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      193 AA
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37, ,193
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Pred. No. 4.7e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IEN-gamma) produce by immunocompetent cells is the product of a phage cDNA clone (T37411) derived from a human liver library. FOR amplification of the CNA (see also T32409 10) and expression in Escherichia coli XI lake MRETKan allowed produced in the countries of the construct hybriders H l. Which produced anti-TEN-gamma inducer protein monoclosal actionable useful in the detection and purification of the inducer protein (see also R9958).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human interferon-gamma inducer protein. IFN-gamma; antiviral: virucide: Interferon gamma inducer protein, IFN-gamma; antiviral: virucide: antitumour; antibacterial; immunoregulator; adoptive ::mmunotherapy
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23-FEB-1995; UP-058240.
10-MAR-1995; UP-078357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A novel human protein (R99564) that induces interferon-gamma
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29-SEP-1995; JP-274988.
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10-NOV-1995; 308055
15-NOV-1994, UT-304:
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Fukuda S, Kohno K, Kunikata T, Ku
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Fred. No. 1.7e 82,
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   TAND AND SELECT OF AND CAUSE AND CAU
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Bost Local Similarity 99.4
Matches 156: Conservative
24 JAN 1996;
04-007-1908;
10-MAP-1095;
29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The mature portion of a novel human protein (89950) induces interferon gamma (IEN-gamma) fields. By immune seperties the distantion of a state of seasons (132404) by immune seperties of a state of seasons (132404) by obtd. From a human liver library. The protein enhances the cytotexicity of killer colls and/or induces the formation of killer cells (e.g., Mx cells, lymphokine-activation (killer (189, cells, and cytotexic T-colls) The mature protein (see also 89958) is useful as an antivital antitumor, antibacterial, immunoregulatory and blood platelet enhancing agent, and can be used in adoptive indumotherapy. It is also used to raise monocional antibodies.
                                                                                                                                                                                                                                                                                                 viral disease; bacterial infection; immune disease
                                                                                                                                                                                                                                                                                                                          Human protein for induction of interferon-gamma Interferos gamma, immunucumpetent cell; malignam
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23-FEB-1995; JP-058240.
10-MAR-1995; JP-078357.
                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                       W24258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                W24258 standard; Protein; 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding interferon-gamma prode.-inducing polypoptide to treat and prevent, e.g. viral disease, malianancies am
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
FUKUDA S. Kohno K. Kunikata T. Ku
Taniguchi M. Tanimoto T. Torigoe K.
WEI. 36:252837/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-SEP-1995;
29 SEF-1995;
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                                                                                                                   17-JUN-1997.
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                                                                                                                                                                                                                                                                     Homo sapiens.
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JP-079357.
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                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                              /note= "Encoded by AYT"
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99.40
40.
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Fred. No. 2.2e-82;
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Best Local :
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Claim 1: Page 9: 12pp; Japanese.

This sequence represents a protein which induces interferon-gamma production in immunocompetent cells. This protein may be used as the major component in a drug for the prevention and treatment of the major component in a drug for the prevention and treatment of
The present sequence represents a newel protein from human cells, which induces interfered gramma (ITM damma) production in immunocompetent cells. This protein chances cytotoxicity of killer cells and induces their formation. It is used as an antioncotic agent for antitumour immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and in the treatment of atopic or immune system diseases, e.g. asthma, hayfever or rheumatism, when formulated with incorlockin-3, it is also used to treat leakopaenia and thromborytopeania associated with radiotherapy or chemotherapy of leukaemia and other cancers, when used in antitumout immunotherapy, this movel protein significantly improves the immunotherapeatic effect of interleukin-2 (II-2), compared with use of II-2 alone either when administered to the medium in which cells (interded for return to the feitent) are being grown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI: 9
                                                                                                                                                                                                                                                                               Human protein that indeeds interferor gamma prode in information color useful for adoptive immuno therapy of tumours and as antimicropial agent etc.
Claim 3, Fage 20, 25pp. English
                                                                                                                                                                                                                                                                                                                                                               (HAYS) HAYASHIPARA SEIRHISH KATAKH
AKITA K. EUJIT M. KHITHOTO M. Nikuda Y. Tanimoto
MPT: 40-205001,414
                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-1996; 336997.
20-SEP-1996; JE-269105.
26-SEP 1995; JC:270725.
29-FEB-1996; JC:270725.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A drug containing a polypoptide which induces interferon-gamma useful for treating e.g. malignant tumours, viral, bacterial o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N.FSDB: I8C209.
A drug containi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiotherapy; immunoregulatory; antitumour agent; chemotherapy; loukopaenia; thrombocytopaenia; immunocompetent cell; asthma; hayfever;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W15701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YEAK ESKI SVIENLNINGVLEIDNINDELFEDMIDSDORDNAPRIIFIISMYKDSOPRGM 60
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97-369391/34.
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⊃e 157 AA:
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73
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77

Matches Query Match

Local Similarity hes 156; Conser

Conservative

99.4\*;

Score 811; DB 1; Fred. No. 2.2e 82; 0; Mismatches 1

Length 193;

0. Gaps

2

51 AVILSVEGETIKITUSGENELIKEENNEEUNIEGIKSCHIEBELEKVEGGENIKKOPTERROSE 1200

1 YFGKLESKISVIENI.NIQVLETIQGANPELEEDMIDSGGFFNAPPITETTSMYKISQPPGM 60

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2
            malignant tumours or viral diseases

Claim 2: Pages 49-50: 74pp; English.

C The present sequence is a protein, which induces

C Interferon yamma (FN quamma) production in immunocomputent cells.

C Interferon yamma (FN quamma) production in immunocomputent cells.

The present has high biological activity, including enhancing expressed in manual resolution by immunocomputent or addition to induction IFN quamma production by immunocomputent cells when expressed in mammalian cells, facilitating its use in cells when expressed in mammalian cells. Facilitating its use in the diseases. As it is expressed in mammalian cells, facilitating its use in containing the used in fections and immune diseases. As it is expressed in mammalian cells, it also has low texticity when used in human treatments, minimising side effects. The DNA encoding the protein can be used in gene therapy, e.g. by injecting vectors containing the DNA or transplanting cells.
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Best Local :
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                                                                                                                                                                                                                                                                                           Genomic DNA encoding polypeptide inducing interferon-gamma production - by immuno-competent cells, useful to treat e.g
                                                                                                                                                                                                                                                                                                                                  N-PSDB: V15825, V15826
                                                                                                                                                                                                                                                                                                                                                      Williamoto M. Okura
WFI; 44-054414/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc_difference 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interferon-gamma production inducer.
Interferon-gamma; TEN-gamma; production inducer; game therapy; immunusummetent cell; treatment; prevention; malignant tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W47429 standard; Protein; 193
Sequence
                                                                                                                                                                                                                                                                                                                                                                   (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Kurlmoto M, Gkura T, Torigoe K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP-815499-A2
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193 AA;
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                                                                                                                                                                                                                                             name inducting polypoptide precursor sequence are IVN damma, precursor, enzyme, clearage
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Fred. No. 1.70 82;
: Misma*ches 1, Indels
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Bost Local Similarity
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                                         enzyme (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma a useful biologically active substance, chancing cytotexicity by and inducing the formation of Aller cells. The
                                                                                                                                                                              Claim 5. Page 15. 18pp; English.
This is the amino acid sequence for the interferon darma (IEN-damma) inducing active protein which is cleaved to form the active mature protein when it is in contact with interleukin-1-beta converting
                                                                                                                                                                                                                                                                                                                                                                            Conversion of interferon inducing polypeptide precursor to active polypeptide - comprises use of interferon-1-beth-converting enzyme useful for e.g. enhancing cytotoxicity by killer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon gamma inducing precursor peptide: IFN-gamma: Interfeuklin I-beta-course ting surges, ICE, egt to winder interfeuklin I-beta-course ting surges; ICE, egt to winder antiseptic antitumour agent; immunopathy agent; antiseptic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 JUL 1997; 365376.
31-JAN-1997; JP-031474.
25 JUL 1996; JF-213267.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W37741;
07 JUL-1998 (first entry)
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30-MAY 1997; JP-156062.
19-JUL-1996; JP-207691.
polypeptide may potentially be used as an antivira).
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WPI, 98 078838/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V18906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurimoto M. Tanimoto T:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JAN-1998.
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Fred. No. 2.2e-82;
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Best Local Fir
Matches 156.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP-821005-A2.
28-JAN-1998.
18-JUDI-1999: 305376.
31-JAN-1997: JP-031474.
25-JUL-1996: JF-210267.
                                                                                                                                                                                                                                         Conversion of interferon-inducing polypeptide precursor to active polypeptide - comprises use of interferon-1-beta-converting enzyme, useful for, e.g. enhancing cytotoxicity by killer cells
This is the amino acid sequence for the interferon-gamma (IFN-gamma) inducing precursor peptide, which is cleaved to form the active mature protein when it is in contact with interleukin-1-beta-converting enzyme (ICE). The polypeptide is used for inducing, e.g. production of IFN-gamma a useful biologically active substance, enhancing cytotoxicity by, and inducing the formation of killer cells. The polypeptide may potentially be used as an antiviral, antitumour and immunogently gament and as an antiseptic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferor-gamma inducing precursor peptide.

Interferor-gamma inducing precursor peptide: IFN-gamma;
Interfeukin-1-beta-converting enzyme; ICE; cytotoxicity; killer cell;
antiviral agent; antitumour agent; immunopathy agent; antiseptic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w37740 standard; Protein; 193 AA.
w37740;
07-JUL-1998 (first_entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HAYB ) HAYASHIBAFA SETRUTSU KAGAKU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cleavage_site
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121 PGYFIA-GEWEPCLEFFLIELKEDELGDRSIMETVANED 157
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YPOKT FORE SVIEWE WALVELING OWER FEEDWIDS FORDWARRITETISMYKDSQERGM 60
                                                                           YEGK: ESKI SVIENI NIMOVIETIMOSNEPLEEDMIDSDORDNAPRITETISMYKDSOPRGM 95
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                                                                                                                                                  Similarity 99.1
56. Conservative
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99.4%: Fred. No. 2.
                                                                                                                                                0; Mismatches
                                                                                                                                                DB 1; Length 193;
3.2c-82;
ses 1; Indels
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tearch completes: June 22, 1999, 10:56:40 Job time: 79 sec

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Match Length DB
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Mutant human inter
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Interleukin 18 act
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Interferon-gamma i
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RESULT
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Colaim 4, pages 38-99, 59pp; English are mouse interfering amma confidence interferon represents the wild-type mouse interferon gamma inducing factors in which one or more cysteline residues are replaced with different residues at or away from the confidence are replaced with different residues at or away from the confidence structure in the confidence with different residues at or away from the confidence of interferon-gamma and are chalmed to be less toxic, more active and stable that the corresponding wild type mIGIF. The modath mIGIFs are also chained to enhance killer cell cytotoxicity and/or induce killer cell of formation, and may therefore be useful as antitumour agents, antitumour remonstberspective, and valved to be useful as antiturous. The companion can also claimed to be useful for trouting hepatitis, or acquired immunophesion services are activities and thrombour period conserved syndrome (ALDS), maluria, takersulosis and of thrombour-period caused by radiation and chemo-therapy.
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Matches 107 Conserv
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03-JUN 1998.

28-NOV-1997; 309632.

14-NOV-1996; JP-329715.

29-NOV-1996; JP-333037.

21-JAN 1997; JP-020906.
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25-SEP-1998 (first entry)
Wild-type mouse interferon-gamma inducing factor.
Interferon-gamma inducing factor.
Interferon-gamma inducing factor, interferon-gamma, killer cell;
antitumour agent; antiviral agent; antimicrobial agent; tumour; migli
antitumour agent; antiviral agent; antimicrobial agent; tumour; migli
hepatitis; malaria, tuberculosis, renal carcinoma; rheumatism; AIDS;
osteopolosis, throubspecia, acquired immunodeficiency syndrome.
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Kurimuto M, Okamoto I. Yamamoto K;
WEI: 38-289-47,26.
N-PSDB; V32755.
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24 NEGELEGITAVIENTNOGULFVEREGEVEEDMIDIEGSASEE, IELIIYMYKKSEVEGIA 60
24 NEGELEGITAVIENTNOGULFVEREGEVEEDMIDIEGSASEE, IELIIYMYKKSEVEGIA 60
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24. .180
/hade= "Matate mouse IS
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                                                                                 R CO. K. KARIBAPA SEIBUISU KACAKU
Karikara I. Kuribera M.
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                                                                                                                                                                   101-10-75 Ref on 101-10-75 Ref on 101-10-75 Ref (841-62)
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eith seelemming estifis, primary hyperthyroidism, osteopenia and
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Fig. 13 Sepp. English.
Fig. 14 (10.18) or a functional equivalent can be used for most estimated to markets. II-18 is used for treating or
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closes lk link, ostoolast, hypercalcaemia, osteopenia,
smooth offs syndrome, ostrosarcoma, arthropathy, osteoporosis,
cmooth offices letoumly ostitis; primary hyperthyroidism
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101 TEN TO THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reptics immunoregulatory; platelet increasing agent; conditional acuminatum, trend cancer; brain cancer; from tiles recumatism, allergy, cyto-taxicity. ALCS, thenkin in the condition of the con
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Mot. The
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                                                                                      Taniquehi M.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antitumour, antiseptic, immunoregulatory and platelet-increasing ages? It can be used for treating or preventing ALDS, condyloma accenting areas or brain cancer, granuloma, mycosis functiones, rhomatism and altergy. The protein can also be used to induce I-Nuamma production in cultured cells. The IFMyamma inducer strongly induces cytotoxicity: I Filler T-colls and when used with interleukin-2 (IL-2) and tumbur necrosis factor (IN-), may improve the effect (or reduce sequence) adoptive immunotherapy in tumburs. The DNA enroding this sequence can be used to produce the protein, which can then be purified (or assayed) sequence 157 AA:
                                                                                                                                                                                                                                                                                                                        22-MAY-1996.
10-NOV-1995; 308055.
15-NOV-1994, JF-304203.
23-FEB-1995; JF-058220.
10-MAF-1995; JF-078357.
Example A 3-2; Page 36-37, 48pp, English.
A novel mouse protein (R99559) induces interferon-gamma (IFN-damma) prodn. by immunocompetent cells. Its sequence was deficed from that of a cDNA clone (T32403) isolated from a mouse liner library.

Recombinant IFN-gamma inducer protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein that induces damma interferon product in immunoccomportent cells - used e.g. as antiviral or antitumour agent, also induces cytotoxicity of killer cells claim 2: Page 22: 30pp: English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1996 (first entry)
Mouse mature interferon gar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the interferon gamma (iffugamma) inducer protein of the invention. This protein induces IFNgamma production in immunocompetent colls. The protein is useful is an intiviral.
                                                                                                                                                                                                                         Fukuda S. Kohno K. Kunikata T. Kurimoto M. Taniquehi M. Tanimoto T. Torigoe K. Ushio S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antitumess, autibacterial, immunoregulator; adoptive immunotherapy
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                                                                                                                                             to treat and prevent, e.g. viral disease, malignancies
                                                                                                                                                              DNA encoding interferon-gamma producing polypoptide
                                                                                                                                                                                       N-PSDB: T32403
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29-588-1935; JE-174388.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 VILSVKDSKXSTLSCKNKIISFEBMDPDENIGGIQSDCIFF_KEVCGGRRBGGESSAYEG 12
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                                                                                                                                                                                                                                            ) HAYASHIBARA SEIBUTSU KAGAKU.
a S. Kohno K. Kunikata T. Ku
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Best Local Similarity 99 4
Matthey 196, Concernative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a protein which induces interferon-gamma production in immunecompotent cells. This protein may be used as the major component in a drug for the prevention and treatment of e.g. malignant tumours, viral diseases, bacterial infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune diseases
Disclosure, Page 10:11, 12pp, Japanese.
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W24262;
IS-00T-100T (first entry)
Murine protein for induction of interferou-gamma.
Interferon-gamma immunocompotent cell; mailynant tumour;
Viral dispase; bacterial infection; immune disease.
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N-PSDB: T80210.
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                                                                                                                                                                   61 VII.SVK158M51LS1EN.11SEEEMMEENIUOIQSOLIFFQKRVPGHNKMEFESSIVEG 120
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                                                                                      RELACQUETOPISTICS SCHOOLS VM PTLINLHOS 157
                                                                                                                                                                                                                                                                                                                                                                    NEGRIBOTTAVIRNINDOVIEVEK ROPVEFEMIOTEOSASEPOTRITTYMYKDSEVRGIA 60
HELACUKEDDAFKLILKKKDENGDKSVMFILINLHQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               containing a polypeptide which induces interferon-gamma for treating e.g. malignant tumours, viral, bacterial or
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157 AA.
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75.07650
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99.4%;
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Fred. No. 1.4e+76,
C. Mismatches 1, Indels
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Sisclosure, Page 22, 25pc, English.

The prosent sequence represents a novel protein from mouse liver cells, the prosent sequence represents a novel production in immunocompetent couls. This protein enhances cytoloxicity of killer culls and induces of their formation. It is used as an antionotic agent for antitumour from the interpresent of their formation. It is need as an antionotic agent for antitumour conditions in the treatment of atopic or immunitarial agent. The interpretation of representation of representation of representation of representation of the protein in antitudent immunitarial accordance in antitudent immunitarial for the immunitarial administration of 11.2) or by addition to the medium in which cells so sequence if it retain the patient of the patient of the patient.
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WPI; 97-205381/
N-PSDB; T60536.
                                                                                                                                                28-SEP-1998 (first entry)
Mouse Lt-18 protein fragment.
Interieuki-18. It 18. murile, treatment, autoimmune diseimmunosuppressant; inhibitor; receptor protein; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAYB
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26-SEP:1995; IP-270725.
29-FER-1996; IP-067434.
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Interferon-gamma, IFM-gamma; antivital; antioncotic; radiotherapy;
immuneregulatory; antitumeur agent; chemotherapy; leukopaenia;
throntwoythpa-nia, immunocompetent cell, asthma; hayfever;
rheumatism; interleukin; killer cell.
                                                                                                                     Mus sp.
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                                                                 Protein
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                                                                                                                                                                                                                                                                                                                W63811
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20-SEP-1996;
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a K, Fujii M, Kurimoto M, Nuk
97-205381/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELACOMESDASET ELEMENSDESVMETETNEROS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VILSVKOSKMSINSCKNKIISESEMDPFENIUDIQSDLIEFQKRVPGHNKMEFESSLYEG 120
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                                                                                                                                                                                                                                                                                                             standard; protein;
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/label= 1L-18
/note= "partial sequence"
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1. .157
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U. Mismatches 1. Indels
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Mittae Interleakin-18 protein (IL-18).
Mittaer (eterleakin-18 receptor, IL-19
Hemide Sy temi "realment: autoimmune:
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contact dy and hybridoma used to detect interleaking
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         Matches
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28-NOV-1997; JP-329715.
14-NOV-1997; JP-329715.
29-NOV-1996; JP-333037.
21-JAN-1997; JP-020906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Motini acroso interferentigamma inducing factor 1131E/MUTII.
Interferon-gamma inducing factor; interferon-gamma, killer rell:
antitumour agent; antiviral agent; antimicrobial agent: thumour; mYGFF;
hepatilis; malaria; tuberculosis; renal carcinoma; rheumatism; AIGS;
astosperessis, thrumbepedia, asquired immunoudeficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a murine interleukin-18 (15-18) gallyper(14-15-16-16-16-18) is a lyn-of-gylot-young properties transduction in immune systems. The interleukin-18 receptor polypoptide can be used to centralise interleukin-18 activity or to treat interleukin-18 receptor susceptive diseases, especially to treat autoliminate or allorgic diseases or as an immunosuppressant. Conditions which may be treated include e.g. graft or organ rejection, pernicious which may be treated include e.g. graft or organ rejection, pernicious anaemia, insulin-related diabetes, discoid lupus erythematosus, allorations, activities, lieutopencia, recuments, Hitch products may also be useful in the freatment of septic shock associated with tensors of the useful in the freatment of septic shock associated with
  Mutants of interferon-damma inducing polypeptide - useful as antitumour, antivital, antimicrobial or anti-immunopathic agents Claim 6; page 44; 59pp; English.

The present sequence represents the mutant mouse interferen-damma inducing factor mIGIF/MUT11. The wild-type mouse interferen-damma
                                                                                                               WP:: 98-288747/26
N-PSDB: V32632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-SEP-1998 (first entry) Mutant moves interferon gas
                                                                                                                                                        Kurimoto M, Okamoto I, Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 42; 51pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-MAR-1997; JP-074697.
28-JUL-1997; JP-215488.
                                                                                                                                                                                                                                                                                                              EP-845530-A2.
                                                                                                                                                                                                                                                                                                                                                                           Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W48968 standard; Peptide; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergic diseases
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                                                                                                                                                                                 (HAYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local similarity 99.4%;
hes 156; conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 VTISVKDSKXSTLSGKNKIISEERMOPPENIOOTQSDLISFQKSVIOGNEMBESSLYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEGELBOTTAVIENINIOVLEVEKKOPVEEDMITTIOZSASETOTET TYMYKOSEVEGLA (*
                                                                                                                                                        ) HAYASHIBARA SEIBUTSU KAGAKU
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                                                                                                                                                                                                                                                                                                                              /mote- "changed from Cys in wild-type to Ala mutant"
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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Pred. No. 1.4e-7h;
The wild-type mouse interferent damma
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                                                                                                                                                                                 Query Math's
Best Local Similarity
Math's 150 Tiver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local :
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EP-861663-A2.
02-SEP-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of engline personal obteoclastoma, Behoet's Syndrome, of english personal obteoclastoma, Behoet's Syndrome, obteoclastoma, obteoclastoma arthitis, deformity ostitis, primary hyperthyroidism and obteoporosis
placiosure; page 34; 56pp; English.
Interlepkinn18 (II-18) or a functional equivalent can be used for inhibition of obteoclast formation. It'l8 is used for treating or presenting estimated diseases a gingeroal capital englishment's syndrome. Asthropathy, phronic rheumatoid managed for treating of presenting syndrome. Asthropathy, phronic rheumatoid managed for the present of the pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W77090 standard, Peptide, 157 W77090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Gillespin MT Harward NT Kirlestoll
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25-EEB-1997: FE-055469
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of lpterleuble 19 to
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                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA;
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Fred. No. 2.9e-76;
0, Mismatches 1, Indels
                                                                                                                                                                                 Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents the mutant mouse interferon-gamma inducing factor midit/MUT12. The wild-type mouse interferon-gamma lactor (midit) sequence is sown in MARANA. The invention provides for motant human and nouse interferon-gamma inducing factors in which one or more cystoine residues are replaced with different recidues at or away from the consensus sequences shown in W48956-W48958. The mutant midiffs are capable of stimulating immunocompetent cells for the production of interferon-gamma and are claimed to be less toxic, more active and stable than the corresponding wild type midiff. The mutant midiffs are also chaimed to whather their overlaying the motant midiffs are also claimed to be useful as antitumour agents, antitumour immunotherapeutics, untiviral agents and artimicrobial agents. The mutant midiffs are also claimed to be useful for treating bepatitis.
                                                                                                                                                                                                                                                                                                                                                                                   acquired immunudeficiency syndrome (AIDS), malaria, tubercalosis, soli mulignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and thrembed enia caused by radiation—and chemo-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutants of interferon gamma inducing polypeptide useful as antitumour, antiviral, antimicrobial or anti-immunopathic agents Claim 6; page 44; 59pp; English.
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Mutant mouse interferon-gamma inducing factor miolE/MUILZ.
Interferon-gamma inducing factor; interferon-gamma, killer cell;
antitumour agent; antiviral agent; antimicrobial agent; thumour; mIGIE;
antitumour agent; antiviral agent; constitution agent; thumour; mIGIE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W48969;
25-SER-1998
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21-JAN-1997;
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                                                                                                                                                                                                                                                      Tocal Similarity
                                                                                  .51
                                                                                                                      61 VT: SVEUSKMSTLSGENKLISES SMORSENJEDI, SELLFRORFWEJENDREBESELYES
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                                                                                                                                                                                               NEGKLHTI IAVIENINIKAVI EVIKERREVEELMIDIINGSASERRIKLIIYMYKDSEVEGLA 50
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                                      HE ACTEDITATELLERENDENGORSVMFTLTNLHQS 157
                                                                                  VILSVELGEMENTISCENEITSEEEMDESENIDFLESSCIEEGEEVDGBRENEEDSSCREG
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HELASOMEDDAFKLILKKMEBNGDKSVMETLINLHOS
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                                                                                                                                                                                                                                                                                                                                                                 157 AA;
                                                                                                                                                                                                                                                        Liarity 90.48;
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                                                                                                                                                                                                                                                        Score 802: DB 1:
Pred. No. 3.7e-76:
Nismatches 1:
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West (Johal
                                                                                                                                           (1.48 ) 1.08800 PR
(1.48 ) 1.080 PR
(1.48 ) 1.08 (2.71 )
W10 R V1.870
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AVTESVKDGEMSTESCKNKIISFE---

120 GHFLACQKEDDAFKLILKKKDENGDKSVMFTLTNLHQS 157

60 AVILSVKDSKMSILSCKNKLISFEEMDEPENIUDIQSDLIFFQXBVPGHNKMEFESSLYE 119

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         quantitating stress in a mammal Claim 6: Page 33: 47pp: English.

This is the amino acid sequence of the rat interferon-gamma inducious factor (GIE) isoform also known as interleukin-18-alpha (II-18-alpha). It can be used to transform a cell, which upon its expression can cause the cell to produce rat INTE, i.e. IL-18 or IL-18 alpha. It is made by the deficient of 57 bases (360-417) from V20875, a probable expo. The antibody to ISTE ISTE and probes derived from it, are useful for detection of II-18 of IL-18 alpha process in a sample. The archivel of IL-18 of IL-18 alpha process.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-SEP-1997; U15891.
08-APR-1997; US-043087
06-SEP-1945; US-025141
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Rat interferon-gamma inducing factor: IGIP; interleukin-18: 11.-18:
IL-18-alpha: transformation: antibody: probe: tybrid:sation.
                                                                                                                                                                                                                                                                                                                                                                         can be used to quantitate stress in a mammal. Sequence 175 AA;
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WPI; 98-193622/17.
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                                                                                1 NEGELHOTTAVIRNINGQVLFVGKEQ-PVEFFMTDIEQSASEPQTEL11YMYKDSEVRGL 5%
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HEGELHOTTAVIESINGAVIEVLEHING TITTAL TITTAL TITTAT TOTAVIEVENEN TOTAVIEVEN TOT
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                                                                                                                                                                                                   77.7%: Score 631; DB 1; Lengti: 175; 79.7%: Pred. No. 2.5e-58;
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90.5%;
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Pred. No. 7.5e-70;
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    Indels 20; Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FI Mutants of interferon-gamma inducing polypeptide - useful as a stillumour, antiviral, antimicrobial or anti-immunopathic agents PS Claim 5; page 41; 59p; English.

On the present sequence represents the mutant human interferon-gamma inducing factor IGIF/MUT21. The wild-type human interferon-gamma inducing factor sequence is shown in W48959. The invention provides for mutant human and mouse interferon-gamma inducing factors (IGIF) in which one or more cysteline residues are replaced with different residues at or away from the consensus sequences shown in W48956-W48958. The mutant IGIFs are cupable of stimulating immunocompetent cells for the production of theerferon-gamma and are claimed to be less toxic, more active and consensus are supable of stable than the corresponding wild type interferon-gamma inducing factor. The mutant IGIFs are also claimed to enhance killer cell cytotoxily analyzer induce killer cell formation, and may therefore
                                                                                                                                                                                                                                                                                                                                                                              Ouery Match

64.88, Score 526, DB 1, I
Best Local Similarity 65.68, Pred. No. 1.7e-47;
Matches 101: Conservative 27, Mismatches 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be useful as antitumour agents, antitumour immunotherapeutics, antiviral agents and antimicrobial agents. The mutant IGIFs are also claimed to be useful for treating hepatitis, acquired immunodeficiency syndrome (AIDS). majarja. tuberculosis solid malignant tumours (e.g. renal carcinoma), thermatism, osteoporosis and thrombopenia caused by radiation—and chemo-therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eccation/Qualifiers
Misc_difference 38
/note= "changed from dys in wild-type to Ser mutant"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W48962 standard: Peptide: 157 AA.
W48962:
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WPI: 98-288747/26.
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29-NOV-1996; JP-333037.
21-JAN-1997; JP-020906.
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03-JUN-1998.
28-NOV-1997: 309632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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Synthetic.
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                                                                                                                                                     120 GHFLAGGKEDDAFKLILKKKDENGDKSVMFTLTN 153
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                                                                                                                                                                                                                                        51 VILSVKOSKMSTISCKNKTISEBEMUPPENIUDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
                                                                                                                                                                                                                                                                                        2 FORTESRUSVIANLNOOVERIOGONA PLABOUMEUSOSKUNAPETIFIISMYKDSOPROMA 61
                                                                                                                                                                                                                                                                                                                                   2 FGELHCITAVIENINGQVLEVUK-ROPVFEDMIDIDQSASEPQIRLIIYMYKDSEVRGLA 60
                                                                                                        GYFLACEKERDLFKLILKKEDELGDRSIMFTVQN 155
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                     June 22, 1999, 10:56:40
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BOOHHHWANDEPBOOHHHWAN BE BOOTHHWAN BENDOCHHW
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1.966 Million cell updates/sec
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Mutant human
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RESULT
R99564
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R92506
                                                                                                                                                                                                                                                                                                                                                                                                                              Protein that induces gamma interferon product in immunicommpetent process; used e.g. as antiviral or antitumour agent, also induces proved in the first profess.

Claim 2 Page 22 3CFp English.

CO This sequence represents the interferon gamma (IFNgamma) inducer protein CO immunocompetent cells. The protein is useful as an antiviral, antitumour, antisoptic, immunoregulatory and plateletinoreasing agent.

CO In the investion immunoregulatory and plateletinoreasing agent.

CO It can be used for treating or preventing AIES, condyluma aduminatum, or real in brain captur, granuluma, nyodise fungacione theuraits and collition of collitors. The protein can also be used to induce TFNgamma production in CO cultured cells. The IFNgamma induces trongly induces anythogolity of hiller Trocals and when led with interleuklic (IL-2) and thouse can be used to immunotherapy in tumours. The DNA encoding this sequence can be used to protein antibodies.

So Sequence 157 AA:
                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                               Matches
                                  29-SEP-1996 (first entry)
Human interferce gamma inducer protein.
Interferce gamma inducer protein: IFN-gamma: antimiral: wirucide:
antilumous, antibacturial. immunutegulator: adoptive immunotherap
therapy: cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interferon gamma production inducer protein.
Interferon gamma, inducer, Invamma, inducer, coll; antiviral:
Interferon jamma, inducer, Invamma, inducer, coll; antiviral:
antitumour; antiseptic; immunoregulatory; platelet increasing agent;
therapy, prevention, studylumn souminatum, renal dancer; brain cancer;
therapy, prevention, studylumn souminatum, alloray, cytotunisity; AIDS;
grantion; mycosis fungitudes; rheumatism, alloray, cytotunisity; AIDS;
killer foell, interfeul in 1.2, Inc. turbur neurosis factor; TMP;
adoptive immunotherapy; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HAYB ) HAYASHIBAKA SEIBUISU KAGAKU.
Kohno K. Kunikata T. Kurimoto M. Okamura H.
Tanimoto T. Torigoe K;
WPI: 96-070177/08.
Homo sapiens.
                                                                                                                                                  E99564 standard, Frotein; 157 AA
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13-JUL-1995; 304906.
14-JUL-1994; JP-184162.
10-FEB-1995; JP-045057.
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02-SEP-1996 (first entry)
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                                                                                                                                  R99564;
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6; Conservative 0; Mismatche
Location/Qualifiers
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Š Š
                                                                                                                     PAYASHIMAPA SEIRUTSH KAGAKU
S. Koho K. Kunikatell, Ko
b. M. Frimero E. Torigoo K
                                                                                                                d: Fire-ent. e.g. viral disease, malignancies and
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                                             out protein
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interferon damma inducer protein, antiviral, virucide,
interferial: immunorequiator: adoptive immunotherapy;
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important cells. It enhances the cytotoxicity induces the formation of killer cells (e.g.
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                                        (R99558) induces interteron-gamma (IEN-damma)
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Toridoo K. Ushia s
                          It enhances the cytotoxicity of
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R99560 ID R9 AC R9 DT 29

R99560; 29 SEP 1996 (first entry)

R99560 standard; Protein; 193

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                                                                                       Query Match
Best Local :
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Best Local Similarity
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22-MAY-1396.
10-NOV-1995; 308055.
15-NOV-1994; JP-304203.
23-FEB-1995; JP-058240.
10-MAR-1995; JP-252062.
29-SEP-1995; JP-274988.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic Treells, especially and cytotoxic Treells, especially can be produced in the produced with a vector carrying the encoding cNA (732402). It is useful as an activitial, antitumor, autibacterial, immunoreculatory and blood platelest chancing agent, and can be used in adoptive immunotherapy. It is also used to raise monoclanal autibodies.
                                                                                                                                                                                                  Example A 3-2; Page 36-37, 48pp, English.

A novel mouse protein (P99559) induces interferon-gamma (IFN-gamma) prodn. by immunocompetent cells. Its sequence was deduced from that of a cDNA colone (T32403) isolated from a mouse liver library.

Recombinant IFN gamma inducer protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse mature interferon-gamma inducer protein.
Interferon-gamma inducer protein; IFN-gamma; antiviral; viruoide;
antitumour; antibacterial; immunorequiator; adoptive immunortherapy;
                                                                                                                                                                                                                                                                                                                                   DNA escoding interfere games producing bulgpoptide to treat and prevent, e.g. viral disease, malignancies and
                                                                                                                                                                                                                                                                                                                                                                                             Taniguchi M, Tanimoto T, Torigoe K, WPT: 96-252837/26.
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                                                                                                                                                                                    carrying the cDNA
                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; T32403
                                                                                                                                                                                                                                                                                                                                                                                                                                 (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Fukuda S, Kohno K, Kunikata T, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-SEP-1996 (first entry)
                                                                   y Match 100.0%; Score 31; DB 1; Tenath 157; Local Similarity 100.0%; Pred. No. 2.5; hes 6; Conservative 0; Mismatches 0; Indels
16 NDQVLF 21
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                                 1 NDQVLF 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             milarity 100.0%; Score 31; DB 1; milarity 100.0%; Pred. No. 2.5; Conservative 0; Mismarches ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= Ile, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurimoto M,
                                                                                                                                                                                                                                                                                                                                                                                                             Ushio S:
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Query Match
Best Local
Matches
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15-NOV-1994; JP-304203.

23-FEB 1995; JP-058240.

10-MAR 1995; JP-078357.

18-NSP-1995; JP-27898.

29-SEP-1995; JP-27898.

29-SEP-1995; JP-27898.

29-SEP-1995; JP-27898.

18-NSP-1995; JP-27898.

18-NSP-1996; JP-27898.

18-NS
                                                                                                 J09157180-A.
17-JUN-1997.
24-JUN-1997.
04-JUN-1997.
04-JUN-1995.
10-MAR 1995.
29-SEP-JOSE.
71-J7857.
  (HAYB )
WPI: 97-
N-PSDB:
A drug o
                                                                                                                                                                                                                                                                                                                 W24262;
15-007-1997 (first entry)
Murius protein for induction of interferon-gamma.
Interferon-gamma; immunocompetent cell; malignant tumour;
interferon bacterial infection; immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6) Page 41-42: 48pp: English.

Claim 6) Page 41-42: 48pp: English. by immunocompotent cells. It is the groduct of a normal product by immunocompotent cells. It is the groduct of a CDNA Clone (132404) obtd. From a human liver library. The protein echiaces the cytotoxicity of killer cells and/or rightness the formation of killer cells (e.g. NK cells) lymphokina artivating killer (ANK) oblis, and hydroxic Tropis) lymphokina artivating killer (ANK) abils, and hydroxic Tropis) antitumor, antibacterial, immunoregulations and blood platelet enhancing agent and can be used in adoptive immunotherapy. It is also used to raise manusclonal antibadies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W24262;
W24262;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding interferon gamma prodm. inducing polypoptide - useful to treat and present, e.u. viral disease, malignancies and immune
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                                                                                                                                                                                                                                                                               _difference
                          97-369391/34.
DB: T80210.
                                                                            ) HAYASHIBABA SEIRHTSH KAMAKH
containing a polypeptide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 100.0%; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 AA,
                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- ile.
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37. ...
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Pred. No. 3.2;
Mismatches
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RESULT W31757 W ACC WIDT TILL LET THE KW ETH KW ETH
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WL4L58
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Best Local Similarity 100.0%;
Matches 6; Conservative 0
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17-J0N-1997
24-301-1996; 028722
14-1071-1996; 1P-279906.
10-MAK-1995; JP-078357.
29-SED 1995; JP-078357.
29-SED 1995; JP-078488.
(HAYE) HAYASHIDARA SEIBUTSU KAGAKU.
WP1; 97-309891.34.
N-PSDB: T80209.
                                                          Homo sapiens.
                                                                                  15-JAN-1998 (first entry)
Interforce gamma inducing factor-2 (ISIE-2) El401 variant.
Interforce gamma inducing factor 2, ISIE-2, Ecocoytt, lyaphwyth, lufilarmathon; grafiferation; differentiation; maturation, tissue dammathon; grafiferation; differentiation; maturation, tissue dammathon; grafiferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          production in immunocompetent cells. This protein may be used as the major represent in a drug for the piecetic and iteration of e.g. molignant tumours, wiral diseases, bacterial infections and immune diseases.
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This sequence represents a protein which induces interior cumma production in immunocompetent cells. This protein may be used as the major component in a drug for the prevention and theatment of e.g. malignant tumours, viral diseases, bacterial infermions and
                                                                                                                                                                                                                           W31757 standard; Protein; 193
W31757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_difference 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              viral disease, bacterial infection, immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human protein for induction of interferon-gamma. Interferon-gamma, immunocompetent cell; mallgnant immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W24258 standard; Protein; 157
Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immune diseases
Claim 1. Fage 9, 12pp; Japanese.
This sequence represents a prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A drug containing a polypeptide which induces interferon vanma useful for treating order mailyment tumours, viral, bacterial o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune diseases.
Sequence 157 A
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Pred. No. 2.5;
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est kesil Samilarity
                                          this is the modern separate inheriteron damma inducing factor-2 (2). Which is a calculate (W175) and an 15H variant (W2049), when may seem a commute fourscript also exist probes derived from the calculationers can be used to quantify the expression of 15H 2 in the start we issociated with inflammation or aberrant expression of 15H 2 in protein can be used to screen for compounds that interior with 15H 2 such as antibodies, antagonists or other indiction (especially ribozymes or antisense sequences) of the communication of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This 3: Face a soperior represents an interferon gamma inducing factor-2 (18-2) and a library this sequence of the 2 and a factor and a library. This sequence of there is an ISTS 2 identified from a T-lymphocyte cDNA library (W22047). In that this is identified from a T-lymphocyte cDNA library (W22047). In that this is identified from a T-lymphocyte cDNA library (W22047). In that this is tound to be changed from Arg to He. A second an Int. which is several to publify the expression of IGF-2 in conditions that are used to publify the expression of IGF-2 in conditions that are used to several to or aberrant expression of IGF-2 fer proton on the used to several tor compounds that interact with the 2 to the infliction (especially in the control was severally a IGF-2 expression or activity. The proton on also be used to disagnose, prevent or treat IGF-2 induction is included in the control of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (- X. N.)
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G. Poleman R. Hawkins PR:
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. (1.18 entry)
. name of form to to 2 (NHF 2) protein.
. (1.18 encounts)
. (1.18 encoun
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especially ribozymes or antisense sequences) of IGIF-2 configuration. The protein can also be used to diagnose, prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dirense, treat or present tissue damage associated
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Too.0%; Pred. No. 3.2;
tive (); Mismatches
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om tikkupridamagn
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W15697

W15697

W15697 standard; peptide; 50 AA

9

1 NDQVLF 6

16 NDOVLE

Query Match Best Local Similarity

100.0%;

Score 31: DB Pred. No. 2.5;

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Length: 157

Matches

Conservative

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Mismatches

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25-SEP-1946; 306997.
20-SEP-1996; JF-269105.
26-SEP-1995; JF-270725.
29-FEB-1996; JP-057434.
                                                                                                                                         tumours and as antimicrobial agent etc.

purpose of the property of the protein from nowes live cells. The present sequence represents a novel protein from nowes live cells. The present sequence represents a novel production in immunocompeter cells. This process inchances cytotoxicity of killer cells and induces their formation. It is used as an aptioncotic meant for antitumour immunotherapy, an antiviral including anti-flavor antibacterial area immunotherapy, an antiviral including anti-flavor cells. 3 it is also used to the appropriate when formulated with incubation 3, it is also used to the appropriate and thrombotypopagia associated with used to the appropriate and thrombotypopagia associated with
radiotherapy or chemotherapy of leukaemia and other caucers. When used in antitumous temporterapy, this posed projets significantly improves the immunotherapoutic effect of interloukin-2 (II-2), compared with use of II-2 alone, either when administered to the patient (before administration of II-2) or by addition to the medium in which crits sequence 157 AA:
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Mouse interferen gamma inducer protein.
Interferen gamma, IFN gamma; antiviral; antion otion radiotherapy:
immuneregulatory duritument agent; chemotherapy; octopacha;
thrombocytopachia; immunocompotent cell; asthma: haytovor;
thrombocytopachia; immunocompotent cell; asthma: haytovor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or treat IGIF-2 induction of proliferation, differentiation or materialion of leucocytes or lymphocytes, especially in relation to tissue duran associated with inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                       (HAYE ) HAYASHIBARA SEIBUTSU KAGAKU.
Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto I:
WPI: 97-205381/19.
                                                                                                                                                                                                                                                                                                                                                       Human protein that induces interferon-gamma production in immuno:competent cells - useful for adoptive immuno:thorupy of
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100.0%; Pred. No. 3.2.
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Best Torol S
Matches 5
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26-SEP 1946: TP-264195
26-SEP 1945: JP-270725.
29-FEB-1946: JP-057434.
(HAYP) HAYPSHIRAPA COLL.
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Key
Miso-difference
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W15701;
26 JAN 1950
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09-APR-1997.
26-SEP-1946: 3.
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26 TAN 1998 (first entry)
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28 TAN 1998 (first entry)
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                       (HAYP) HAYPSHIPAPA SEIBUISH KAGAKH
AKILA K. EUJII M. KALIMUTO M. Nekada Y. Tanimoto T
WPI: 97-205381/19
Usman profess that indices (cherferin-garma profession that indices)
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tumours and as untimicrobial agent etc.
Claim 3: Page 19: 26pp: English
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     tumours
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The present seprence represents a sivel protein from howar belief which in hower liberterm judned ITM jurney production in howar belief the formulation of the protein state of the protein of the protein and induced their formulations. It is seen as at these the investigation of antity and activitie (stated as society of actions of the present of atopic or inmune system diseases, et as the concern hayfever or rheumatism. When formulated with interleaking, it is also used to treat leukopaenia and thrombouyupaesia associated with concern the protein and interleaking the contituency improves the formulation of the pattern before soficiently in the pattern before squence 157 AA;
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Wil 98-018522/02.

N-PSDR: V05368: V05368
Antigration of Suran interlection 1 gamma inmunity of the January Surand by human inmunity of Pages 54-55; 63pp; English.
                                                                                                       16 MAY 1997, UCT182.
20 MAY 1996 US 651998.
(SCHE ) SCHERING CORP.
Paran IF Hardhar of Kastelelo
MF11 98-018512702.
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2446592;
244A8Y 1308 (first ontry)
Amino sold sequence of burde interleukin-1-gamma.
Interleukin 1 gamma: II-1-gamma: movies optoblino, ISIE.
Industino, antibody, disjonatic assay: fusion proceins a
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     tta escribbat potypopride inducing interferon damma.
Resolve symmetric myesterit cells, useful to treat e.g. human
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class sigh biological activity, including enhancing
cold viller cells and inducing killer cell formation.
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Best Local Similarity
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18-JUL-1997: 305377.
30-MAY-1997: JP-156062.
19-JUL-1995: JP-207591.
                                                                                                                                                                                                                                         This polypeptide induces IEN-yamma production in immunocompetent relis (the polypeptide is not named but is described in the 2016/96 and 19309/96.) An engine it there is the present form of this polypetide into this active form by cleaving a linkage between Asp at amino acid position is and Tyr at amino acid position 3.5 the precursor. The cusyme can be obtained from a human harmatopoleric cell and can be inhibited by indesectamide and acetyl-fityresyl-fively-fitalanyl-fit aspartified. The engine can be used for cleaving a recombinant HIN-damen propolypeptide to form a mature polypeptide.
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Misc_difference 73
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10-JUN-1998 (first entry)
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Claim 20: Page 17: 18pp; English.
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RESULT 3 WMVZ14 14K ceil fusion protein - vaccinia virus C:specios: vaccinia virus C:bate, 31-Mar-1989 #seguenoc_iccisio [1-Mar-1989]	Oy 1 NEOVLE 6	guery Mater Best Local Similarity 83.3%, Fred. No. 3.5; Matches 5; Conservative 1. Migmarchy	RESULT 2  G64005  hypothetical protein Higgs Higgs Higgs Lifts Sifts Species: Remophilius Inflaunce C;Species: Remophilius Inflaunce C;Accession: G64005  R;Heischmann, R,D; Adams, M,D; White, C; Tily T, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, F, Lin, Gi, , Socayne, J,D; Soott, J, Shilley, Venter, JC.  A;Arthors: Coston, M,D; Utcerback, T,S; Handa, H,D A;Reference number: AAAnno; MHID;95380630  A;Reference number: AAAnno; MHID;95380630  A;Reference number: AAAnno; MHID;95380630  A;Reference number: AAAnno; MHID;95380630  A;Recidues: Lise HIGE. A;Residues: Lise HIGE. A;Cross: Fellichoses: Gs:Giffilm Lise HIG304  C;Superiamily: hypothetical process HIGGS	Ouery Match 100.0%; Score 31; DB 2; Hest Local Similarity 100.0%, Fred. No. 2.1; Matches 6; Conservative 0; Mismatches (y i NUOVLF 6	ul, H.; Komacsu, I.; Iucsudo, e. 995 a now cytokino that induces IFN S50225  Y X KA KA KA KA EMELICARIANI MIT GINARELL FII	(house mouse) quence_revision 19.	ALIGHMENTS	40 20 83.9 221 2 876055 41 26 83.9 110 2 001833 42 25 83.9 110 2 101833 43 25 83.9 110 2 170451 44 25 83.9 422 2 F64651 45 25 83.9 282 2 834965
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Query Match
Best Local Similarity
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A:Molecule type: mRNA
A:Residues: 1-764 -MOYS
A:Cross-references: GR:M73780: NID-g194520 PTP-g184521
                                                                                                                                                                                                                                                                                         ReMoyle, M.; Napier, M.A.; McLean, J.W.
J. Biol. Chem. 266, 19650-19658, 1991
A:Title: Cloning and expression of a divergent integrin subunit beta-8.
A:Reference number: A41029; MUID:92011767
A:Accession: A41029
G:Superiamily: integrin beta chain 
G:Keywords: cell adhosion: sytoskeleton; duplication, extracellular matrix; diycoprot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C)Species: Homo sapiens (man)
C)Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #rext_change 08 Sep-1997
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C:Superfamily: yeast cytosolic phenylalanine--tRNA liquse alpha chain
C:Keywords: aminoacyl-tRNA synthetaso: ligase: protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: A41029
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A:Authors: Borndovsby, M.; Klonk, H.F., Flaser, C.M.: Smith, H.C.; Wocse, C.R.: Vente
A;Tille: Complete genome sequence of the methanogenic archaeon, Methanococcus Januasc
A;Reference number: A64300 MnTp-06737999
A;Accession: C64438
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C.Accession: C64438

R.Bull, C.J.: White, O. Olson, G.J.: Zhou, L., Eleiselmann, R.D.: Sutton, I.G.: Blak R.Bull, C.J.: Overbeek, R.; Kirkness, E.F.: Weinstock, K.G.: Merrick, J.M.: Glodek, rson, J.D.: Sadow, P.W.: Hanna. M.C.: Cotton M.D.: Poberts, R.M.: Hussl. M.A.: Faine
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A:Residues: 1-548 /BUL>
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A; Molecule type: DNA
A; Mosidines 1:13¢ :354.
A; Coross references: EMBL: M37086; NID:g335300; PID:g435301
A; Coross references: EMBL: M37086; NID:g335300; PID:g435301
C; Superfamily: vaccinta virus 14K cell fusion protein
C; Korwords: glycoprotein; membrane fusion
F:2-136/Product: 14K cell fusion protein: #status predicted <MATS
F:2-136/Product: 14K cell fusion protein: #status fusion fusion
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Best Local Similarity 83.3%;
Matches 5: Conservative
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90 %; Score 28; DB 2, ixmoth 548;
Local Similarity 83.3%; Pred. No. 37;
hes 5: Conservative 1; Mismatches 6; indoes
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Pred. No. 7.6;
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Score 18; Pred. No.

DB 2;

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fusion protein, 14K - Dotromelia virus
C:Species: Entremelia virus
C:Species: Entremelia virus
C:Date: 05 Jun 1331 #Sequence_revision 26-May-1995 #text_change 08-Se
C:Accession: $37282
R:Moyor, H:: Osterileder: X:Y.Z.: Coorny, X:Y.Z.
A:Reference number: S:37274
A:Accession: $37282
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C:Species: vaccinia virus
C:Date. 20:Feb-1991 #sequenc_recision 20-Feb-1995 #text_change 08-Sep-1997
C:Accession: $29911
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A;Cross:16ferences, EMBL.X57318, NID:g62279; PID:g62244
C:Superfamily, vaccinia virus 14K cell fusion protein
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A;Accession: $29911
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A:Residues: 1:110 KNEY
A:Residues: 1:110 KNEY
A:Rotus: references: EMBL.X75157; NID:g404280: PID:g404281
A:Note: the source is designated as mousepex virus
C:Superfamily: "accinia virus 14K cell fusion protein
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                      fusion protein, 14K · monkeypox virus

C:Species: monkeypox virus

C:pate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

R:pate: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Jan-1995 #text_change 08-Jan-1995 #text_change 08-Jan-1995 #text
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A; Statue: preliminary
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es 5; Consort
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Fred. No. 6,
1, Mismatche
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A;Molecule type: DNA
A;Residues: 1 110 <MEY>
A;Cross-references EMBL X75155; NTD:g404278; DID:g404279
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C:Accession: S37274
R:Meyer: H., Ostorriodor, X.Y.Z.: Chorny, X.Y.Z.
submitted to the EMBL Data Library, September 1993
submitted to: identification of binding sites for noutralizing mabs.
A:Description: identification of binding sites for noutralizing mabs.
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C:Superfamily: Vaccinia virus 14% cell fusion protein
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C;bate: 06-Jag:1935 #sequence_iccis: or re-Jag:1745 #text_ctade: 09-986-1007
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A)Cross-references: EMPL-X75156, RTT 3464261, FTT 3464262
C:Superfamily: Macoinia Wirus 148 0-11 (asida piotótio
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probable membrane protein budos - Escherichia coli
C:Species: Escherichia coli
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"Thomas to 1.21; 100002; 18702; S18703
B.F. decors: ".M. Cheraphe, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.;
M.: Foltowinn, T. Nichen, D.; Hiterback, T.P.; Saudek, D.M.; Phillips, C.A.; Merrick,
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Problem 1997 File File Kert (11, G.: Bloch, C.A.: Perna, N.T.: Burland, V.: Riley, M.: Co.
A.: Problem 1977, 1994 134-2, 1997
A.: Problem 1977, 1994 134-2, 1997
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A:Cross-references: EMBL:X17617: NIC:g55470; FID:g55470
C:Keywords: DNA binding: transcription regulation; zinc finger
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A:Residies: 1:580 cculs
A:Cross-references: GB:J04770
R:Cunliffe, V.; Koopman, P.; McLaren, A.: Trowsdale, J.
EMBO J. 9, 197-205, 1990
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Title:

US-99-030-061:2

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Searched: 180763 seqs, 55169189 residues

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## SUMMARIES

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                               W.C. SHIGHERY M.E. HASSHER D. HOFFMAN G. R. KOST T.A. SHEN W. W.C. SHIGHERY M.E. HASSHER D. HOFFMAN G.R. KOST T.A. SHEN W. AND THE M. MCCANLEY P. MCSERHAN G. MITCHELL T. M. SAHET T. M. SHOPPEN M. SPATION T. K. SHORNEN F. SPATION T. M. SAHET T. MILLARY D. BECHERER J.D. STATE M. MILLARY D. BECHERER J.D. SHORNEN F. SPATION T. MILLARY D. MILLAR
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SPORAS METADOAS MERBAJAS VEKTERRATAS MARMALIAS EUTHERIAS PRIMATESS
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Ed (92/07) (F)
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HIBERTALIDAE: HOMO.
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83.48;
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LAST SECTION OPDATE)
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Frod No 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prod. No. 31:
Prod. No. 31:
L: Mismatches 0: Indels
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                                                                                                                                                                                                                                                                                                                                                                               027196
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Best Local Similarity 83...
School 5: Conscryative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Trakes 5: Conserv
                                                                                                                                                                                                                                                                                           027196;
027196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C98726 PPELIMINARY: PRT: 827 AA. 088726; O1-NOV-1998 (TREMBURFI O8, CREATED) O1-NOV-1998 (TREMBURFI OR, LAST SECUENCE "PDATE) O1-NOV-1998 (TREMBURFI OR, LAST ANNOTATION UPDATE) ON-NOV-1998 (TREMBURFI OR, LAST ANNOTATION UPDATE) THE-AITHA CONVERTING ENZYME (IACE) PRECURSOR (IACE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                               01-JAN-1998 (TREMBLPEL 05, 01-JAN-1998 (TREMBLREL 05, 05, 01-AUG-1998 (TREMBLREL 07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

AMOUR A., SICCOMBE P.M., WEBSTER A., BUTLER M., KNAYDER V.

SMITH B.I., STEPHENS P.E., SHELLEY C., HUTTON M., KNAYDER V.

DOCHERRY A. I.P., MURPHY G.;

"The TNF-alpha converting enzyme ADAM-17 is inhibited by TIM

STEPHENS. TO FMBL/GENRAME/TOBJ EALA FAMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLACK P.A. PAUCH C.T. KOZLOSKY C.J. PESCHON I.J. SLANE I.I. MOLESON M.F. CASTNER B.J. STOCKING K.L. KELDY F. SKINIVASAN K. RELESON N. BIOANI N. SCHOOLEY K.A., CEHHART M. DAVIS R. FITZNER J.N. JOHNSON F.S. FANIUN B.J. MARCH C.J. CEKRETI D.F. A metalloproteinase disintegrin that releases tumour-nocrosis factor alpha from cells."

(actor alpha from cells.")

(actor alpha from cells.")

(actor alpha from cells.")

EMBL: U8675; G1857673; --

EMBL: U869612; G2039383; --

EMBL: U69612; G2039383; --
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EUKAFYOTA: METAZOA: CHORPATA: VERTEBBATA: MAMMALLA: EUTHERTA:
RODENTIA: SCIUROGNATHI: MUFIDAE: MUFINAE: MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE: 97186574.
ARCHAEA: EURYARCHAEOTA: METHANOBACTERIALES; METHANOBACTERIACEAE
                                            METHANOBACTERIUM THERMONUTOTROPHICUM
                                                                                                                                SENTORY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00099; zn-protease; 1.
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                                                                                                                       TRANSPUCTION HISTIDINE KINASE
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17
827 AA:
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22
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                                                                                                                                                           CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Fred. No. 84;
1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL:
TNF-ALPHA CONVENTING ENZYME (TAGE)
: C9DEA655 CRC32:
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Best Local s
Matches
Query Match
Best Local Similarity
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Q23078: PREMBUREL 01...
Q1.WV-1396 (TREMBUREL 01...
Q1.WV-1000 (TREMBUREL 08...
                                          SEQUENCE TO NO.

STRAIN-BRISTOL NO.

WAITERSTON R.:

SUBBLITTED (JUL-1996) TO EMBL/WERBANK/DUBG DATA BANKS
EMBL: U54840; S1465791; -...

THOUSENER 308 AA: 34316 MW: E433004A CRC32:
                                                                                                                                                                                                                                                                                                                 WILSON R. AINSCOUGH P. ANDERSON K. BAYNES C., BERKS M., BONFIELD J.
PORTER J. CONSET M. CORSEY T. COLORER J. A. CREAN M.
DEAR S. DO Z. CHERN F. FAVELLO A. FULTON I. GAFONES A., GREEN P.
HAWKINS T. HILLIEF I., JIEF M., JOHNSTON I. MONES M., KEESHAW J.,
KEESHAW J.,
MONHPRAY A. MORTHORPE B. O. COALLACHAN M., PARSONS J. PEPCY C.,
BISKEY J. FOSEA J. SAINDERS C., SHOWNKEEN F., SMALLON N., SMITH A.
SONNHAMMER E., STADEN R., SULSTON N., THERRY-MIEG J., THOMAS K.,
VANIDIN M. VANIGAN K. WAREFSTON J. THERRY-MIEG J., THOMAS K.
WILLKINSON-SPROAL J., WORLDMAN P.,
WILKINSON-SPROAL J., WORLDMAN P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAENORHABDITIS ELEGANS.
EUKARYOTA: META7:A: NEMATODA: SECEPNENTEA: PHAROITIA: PHABDITIDA:
EUKARYOTA: WETA7:A: NEMATODA: PHABDITIDAE: PELODERINAE: CAENORHARDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTHER PROPERTY STAMM I A LEFT-OUGHERY C LEE H.-M., DOBOIS J. ALTERDAR P. MARKEY D., COUR D. GILBERT K.
HARRISON D. HOANG I. KRACIE P. LIMM W., POTHER B. QIU D.
KRACIE P. LIMM W., POTHER B. QIU D.
KRACIE P. LIMM W., POTHER B. QIU D.
KRACIE P. LIMM W., POTHER B. QUI D.
KRACIE SALTE B. SALTE B. SALTE D. FRANKAN S., MIDCUGALL S.
KHIMER G., STYAL A. PITT-POVERI S. CHUPCH G.M., DANIELS G.J.,
MACO I. FICE P. NOTHING J. REEVE J.N.,
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STRAIN=DEL
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EMBL: AEQCORS: CREEZEZT: -
EMBL: AEQCORS: CREEZEZT: -
SEQUIENCE 348 AA: 39301 MW: 04ABABEE CRO32;
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MILSON R. AINSCOUGH R. ANDERSON K. BAYNES C. BERKS M. BONFIELD RIPETON I COUNSIN A. CHANTON M. FRETON I COUNSIN A. CHANTON M. TEAS S. P. S. PIPETN P. FAVELLO A. FILTON I GARRIER A. GERLA HAWKINS T. HILLIER L. JIER M. JOHNSTON L. JONES M. KERSHAW J. KIRSTEN T. LAISTER N. LAIFFILLE D. LIGHTINNS J. LIOYD C. MCMURRAY A. MOPTIMOPE B. CICALLAHAN M. PARSONS J. PEPCY C. MCMURRAY A. MOPTIMOPE B. CICALLAHAN M. PARSON S. PEPCY C. HIFKEN L. MCMAFA A. SAUNLERS C. SHUMKKEIN E. SMALDON N. SMITH SONNHAMMED B. STAFEN P. SUISTON J. THIEFPY MIEC I. THOMAS Y. WILKINSON-SEPCAN F. WOHLDMAN P. MILKINSON-SEPCAN F. WOHLDMAN P. MILKINSON-SEPCAN G. WOHLDMAN P. MILKING G. WOHLDMAN G. WOHLDMAN P. MILKING G. WOHLDMAN G. WOHLDMA
                                          CAEMOPHARDITIS ELEGANS.
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CARRING M., CRAXION M.,
CREEN F., CARRING M., CRAXION M.,
CREEN F., CHRISTON L., JONES M., KERSHAW J.,
LATHELLE F., LICHTNING J., LLOYE C.
F. FIRMARE B., COALLAHANN M., FARSONS J., FERRY C.
F. FIRMARE B., COALLAHANN M., FARSONS J., FERRY C.
F. FIRMARE B., CRALLAHANN M., FARSONS J., FERRY C.
F. FIRMAN M., SATURERS D., SHOWNEEN R., SMALDON N., SMITH A.
B., STANDAN K., WALTENTON R. WATTON A. WEINSTOCK L.
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SCHYIES: SLEFMAT-PHYTA; MAGNOLIOPHYIA:
AE: "TAF-ARALES: BRASSI"ACEAE; ARABIDOPSIS.
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ALIENSCHMIDT 0. BOKRANZ M., FUCHS G.;
*Nove) actuble 2 aminobenzoate metabolism. Nucleotide serpence of
*Nove) actuble 2 aminobenzoate metabolism. Nucleotide serpence of
plasmid carrying the gene for the flavoprotein 2 aminobenzoy: "OA
monocxygenaso/reductase in a denitrifying Pseudomonas sp.";
ECR. J. BIOCHEM. 2071: 12 FLZ (1992).
-1- SIMILARITY: 10 GENE 11 AND X PROTEINS (P154.9) FROM
BACTERIOPHAGE 12-2.
EMPL. MITTER S24378.
HYPOTHETICAL PROTEIN: PLASMID.
SECTENCE 372 AA. 42562 MW. 44330571 GROSS:
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61-JAN-1998 (TREMBUREL 05, LASI SEQUENCE OPDATE)
01-N-V-1998 (TREMBUREL 05, LASI ANNOTATION UPDATE)
RESISTANCE COMPLEX PROTEIN 12C-2.
12C-2.
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01-NUV-1996 (TREMBLEEL 08, LASI SEQUENCE UPDATE)
01-NUV-1998 (TREMBLEEL 08, LASI ANNOTATION UPTATE)
HYPOTHELICAL 42.2 KD FROTEIN (ORF 5).
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PEAM: PE00931: NB-ARC: 1.
SECUENCE 1240 AA. (41523 MW: 15839309 CRC3.
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"The 12C family from the wilt discuse resistance locus 12 belong
the nucleotide binding, leucine-rich repeat superfamily of plant
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EURAPY TA: VIPILIBLANIAE: CHAROCHYLA/EMBERGHRIA GEGOT: EMBERTHRIA:

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EURICOTYLEBOORS: ASIEBILDAE: SCLANNANAE: SCLANNALES: XCLANACDAE: SCLANNANES
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PLASMID PKB740.
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PLANT CELL 9:521-522(1997).
EMBL AP004879; G2258317; -.
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ENVELOPE PROTEIN.
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SEQUENCE 92 AA:
  01-NOV-1996 | 076989;
01-NOV-1996 | 076989;
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077073;
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"Two different deles account (Electrontic binding proteins in Staphblocous delesses. The complete nucleotide sequence and characterization of the second gene.";

FIRE T RICHEM 2021041-1048(1991)

EMBL MEGGAGINERA 2021041-1048(1991)

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EMBL MEGGAGINERA 2021041-1048(1991)
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SUBMITTED (JUL-1996) TO EMBL/GENHANK/DDBJ DATA BANKS
EMBL: 276336: E254051. -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-PATIENT MOTHER 566, 24-MONTH SAMPLE;
SIMONON A KAMPINSA G.A. VAN DE PEPRE P., KAPITA E., MSELLATI P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN IMMUNOSEFICIENCY VIRUS TYPE 1 (HIV-1).
VIRUSES: FETROID VIRUSES: REIROVIRIDAE; LENTIVIRUS
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01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLREL, 01, LAST ANNOTATION UPDATE)
ENVELOPE PROTEIN (FRAGMENT).
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BACILLUSA'LASTRIFIUM GROUP: BACILLACEAE;
STAPHTLOCOCCUS.
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71-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
71-NOV-1996 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
FIRECHECTIN BINDING PROTEIN B.
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SUBMITTED (2VI-1996) ID E
EMBL; 275033; ED23624; -
PFAM; PP00516; GP120; IL
ENVELORE PROTEIN.
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KAMPINGA G A , VAN DE PERRE P.,
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OM protein - protein search, using sw model
June 22, 1999, 10:56:39: Search time 61.72 Seconds (without alignments)
2.294 Million cell updates/sea
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Copyright (c) 1993 - 1998 Compugen Ltd.
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Title: Perfect score: US-09-030-061-3

Sequence: Scoring table: BLOSUM62

162000 enge. 20225220 residues

Database . A\_Geneseq\_34:\*

Pred No is the curker of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

## SUMMARIES

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RESULT 2  R99564 Standard: Frotein: 157 AA.  ID R99564; Girst entry)  DE Human interferon-gamma inducer protein.  KW Interferon-gamma inducer protein: IFN-gamma  KW thorapy cancer.  OS Home sapiens.  Fill My sapiens.	Open 1 Match 100.0%; Score 33; 3 Host Local Similarity 100.0%; Prod. No. 2 Matches 1 Matches 7 PKLILKE 7 132 EXCILER 138	RESULT 1  10. 26250; standard, Frotein, 157 AA.  AC 82550;  BT 02.58E+1996 (first entry)  DT 02.5EE+1996 (first entry)  DT 10.5EE+1996 (first entry)  Entricic organia, induces, IENamana, innuvaccompetent cell; antiviral;  KW 20.5EE+1996 (first entry)  ENTRY entricic years and administration fredai value; induces;  KW 20.5EE+1996 (first entry)  ENTRY entricic years and administration fredai value; induces;  ENTRY entricic years and antiviral;  ENTRY entric years and interfered first entric years and production in the invention of the invention. This probe in induces in an antiviral; incompetent teris in the interfered first entric years and places in the invention of the invention of the invention of the invention of the probe in the invention of the invention of the invention of the invention of the probe in the invention of the invention of the probe in the invention of the probe invention of the problem invention of the invention of the problem in the invention of the invention of the	45 33 100.0 157 1 W77158 ALIGNMENTS
a) antiviral; viruside: . uleptive immunotherapy:	B 1: Length 157:	platelethioreasing agent:     renal cancer, hair cancer:     libray: yestekning Richer:     locarsis Easter: TWF:  29.  20.  20.  20.  20.  20.  20.  20.	Human interleukin-

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A board human protoin (R9954) that induces interferon-gamma (FN samma) produce by immunocompetent cells is the product of a class what clone (T241) derived from a human liver library.

FY sumplification of the cDNA (see also T2400-10) and expression in Escherichia coil XL-1 Rive MRF/Kan allowed produced argument thereof protoin. This was used to construct hybridoma H-1, which produced anti-IFM damma inducer protein monoclonal antibody H-ImAh (sector) in the detection and purification of the inducer protein sector.
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Taranah M. Lambusto T. Forlaro K.
Wil of 2024-0720 N. P. 204-11
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**Term tumma inducer protein; tEN-gamma; antiviral; virueide;

**Term un'ibacterial; immunorequiator; adoptive immunotherapy
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                                                                                                                                                                                                                                                                                                           Time 1 48pp: English
                                                                                                                                                                                 William 1, 2200. ...
White in the second sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse ompotent colls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 AA
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.Tp 488215.
.Hr 47835.7.
and it induces the tormation of killer cells
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147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1001,0%; Servic 43: DB 1:
1001,0%; Prod. No. 2.3;
100: 11 Mismatches 0
                 induces interfered damma (IEN damma)
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R99560

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29-SEP-1996 (first entry)

R99560:

R99560 Standard: Frotein: 193 AA.

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Query Match
Best Local Similarity
Traches 7, Conserva
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                                                                                                                    Query Match
Best Local Similarity
Matches 7 Conserv
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15-NOV-1994: JP-304203.
23-FEB-1995: JP-058240.
10-MAR-1995: JP-078357.
18-SEP-1995: JF-262062.
29-SEP-1995: JP-274988.
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22-MAY-1
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                                                                                                                                                                                                                                                                                                                                       Example A-3-2: Page 36-37: 48pp: English.

A novel mouse protein (R3955) induces interferon damma (ifficialization produced from produced from the produced from the sequence was deduced from that of a cDNA clone (T32403) isolated from a mouse liver jibrary. Recombinant IFN-gamma inducer protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a vector coline transformed with a vector colline transformed with transformed with transformed with transforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukuda's, Kohno K, Kunikata T, Kur
Taniquchi M, Tanimoto T, Toriqoe K,
WPI: 96-25927/26.
N-PSDB: T32403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Interferon-gamma inducer protein: IFN-quamma; untivitual: viracijo: antitumour: antibacterial: immunoregulator, adoptive immuno/lerupy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-SEP-1996 (first entry)
Mouse mature interferon-gamma inducer protoin.
                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                      carrying the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding interferon gamma production polypeptide - useful treat and prement, e.g. wiral digease, muliquancies and immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.
Fukuda S, Kohno K, Kunikata T, Ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 FKLILKK 140
132 FKLILKK 138
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                                                                                                          100 0%: Score 33: DB 1: Length 157:
illarity 100.0%: Prod No. 2.3;
Conseivative 0: Wiemm+shire
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Ile, Thr
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Best Local S
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04-0CT 1995)
10-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6. Page 41-42, 48pp; English, protein (p2955) indices interferon gamma (IFN gamma) profus by immunocompetent cells. Interferon gamma (IFN gamma) profus by immunocompetent cells is the product of a cona clone (T22404) obtd. from a human liver library. The protein enhances the cytotoxicity of killer cells and/or induces the formation of killer cells. (e.g. NE cells, and/or induces the formation of killer cells and cytotoxic T-cells) lymphorino-ortivating killer (LAK) cells, and cytotoxic T-cells) The mature protein (see also R99558) is useful as an antiviral, antitumor, antiborterial, immunoricydiatory and blood platelet enhancing agent and can be used in adoptive immunotherapy. It also used to raise monoclonal antibodies
N\text{-}PSDB\text{-}\ TEC210 . A drug containing a polypeptide which induces interferon-gamma
                                                                                                                                                                                                                                                                                                                                                                                                    Murine protein for induction of interferon-gamma. Interferon jamma immunecompotent roll, malignant tumour, viral disease, bacterial infection; immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HAVE ) HAYASHIRAMA SEIBUTSU KAGAKU.
FUKUGA S. KONDO K., KURINTE E., KURINGTO M
Taniquochi W., Taniaoto T., Turique K., Ushio
WPI: 96-25007.756
N.PSOB. TV2404.
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Interferon gamma inducer protein, IFN-gamma, autiviral; vizucide;
anti-umour, a-ribactorial: immunorogulator; adoptivo immunorherapy;
thorapy: cancer.
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus.
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trat and prevent, e.g. viral disease, malignancies and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-712931-A2.
22-MAY-1966.
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                                                                                            (HAYB
                                                                                                                                                                                                                                                                                                                          misc_difterence
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                                      3 ) HAYASHIBAPA SETPUTSU KAGARU
97-369391/34.
DB: TEC210.
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                                                                                                                       020722.
UP-279906.
UP-078357.
UP-274988
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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37. .193
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Pred. No. 2.8;
Mismatches of
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RESULT
W31757
LD W3
AC W2
DT 15
DE If
CREATE AND W3
EH KW 15
EH KW 15
FT M3
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Hest Local Similarity
Technes 7: Conserve
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                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7, 765533
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17-UON 1397
24 JAN 1397: 018711
04-001-1995: JP-279906.
10-MAR-1995: JP-078357.
29-SEF-1995: JP-078357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HAYP ) HAYASHI
WPI; 97-369391/
N-PSDB; T80209.
                           Homo sapiens.
                                   Interferen gamma inducing factor 2 (IGIF-2) R1401 variant. Interferen gamma inducing factor 2, IGIF-2, leucocyte, lymphocyte; billefilmmyfic. priliferation differentiation, materalico, tilluculam.
                                                                                                     W31757 standard; Protein: 193 AA. W31757,
                                                                                                                                                                                                                                                                                                                                                              This sequence represents a protein which induces interferon-gamma production in immunoscupteto tells. This protein may be used as the major component in a drug for the prevention and treatment of equality manufactures, viral diseases, bacterial infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human protein for induction of interferon-gamma. Interferon-gamma: immunocompetent cell; malignant tumcur:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A drug containing a polypeptide which induces interior useful for trooting e.g. malignant tumeurs, wiral, bar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           viral disease; bacterial infection; immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure Fage 10 11, 12pp, Japanese. This sequence represents a protein which induces interferon-damme production in immunocompete the first first protein may be used as the major component in a drey for the provention and treatment of e.g. malignant tumours, viral diseases, bacterial infections and
Misc_difference 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W24258 standard, Fretein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful for treating e.g. malignant tumours, viral, bacterial immune diseases % \left( 1\right) =\left\{ 1\right\} 
                                                                                       15-JAN-1998 (first entry)
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Sequence 157 A
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Claim 1, Faje 9.
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9)-369391/34.
                                                                                                                                                                                                                                                                                                                                      diseases.
ce 157 AA;
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            Location/Qualifiers
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                                                                                                                                                                                                                                                          100.0%,
100.0%;
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Prod. No. 2.3;
P: Mismatthes
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in may be used as
and treatment of
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this is the protein sequence of interferon gamma inducing factor-2 (1918). As PERSON against (W31757) and an IGIF variant (W22049), which may be an alternate transcript, also exist. Probes derived from the color as equences can be used to quantify the expression of PERSON in which can be used to quantify the expression of the expression of PERSON and that are associated with inflammation or aberrant expression of PERSON protein can be used to screen for compounds that the enterministic contacts an indicate the expression of the protein can be used to screen for compounds that the enterministic compounds or antibodies, antagonists or other unline loss (expression of the protein can also be used to diagnose, previous to the protein can also be used to diagnose, previous transfer and the diagnose previous contacts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Has previous sequence represents an interferon gamma inducing tactor-2 (1952) until sequence in the form a liver cDNA library. This sequence striets in the form a T-lymphocyte cDNA library (M22047), the first sequence striets in the form a first sequence striet sequence striets. As a second to be changed from Arg to Ile. A second variant, all 41 is so mais's probes degrees of IGFF-2 in conditions that are used to quantify the expression of IGFF-2 in conditions that are used to death inflammation of abertain expression of IGFF-2 are probes to used to screen for compounds that interact with IHE 2, into an antibodies, antagonists or other inhibitors (especially inform a subject of sequences) of IGFF-2 expression or artifity. The following sequences of IGFF-2 expression or artifity the strict is set in a discussion of diagnose, properties that IGFF-2 induction of problems in the strict in the sequences.
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BG. Therand Bull
97-30 of Nazari
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    I depress does not appear in the specification, it has
the large the LUF 2 sequence presented in W22047.
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                                                                                                                                                                                                                                                             There dumma inducting factor-2 - used to screen the dumma inducting factor-2 - used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number inducting factor-2 (1318-2) protein.
number inducting factor-2: 1318-2: leucocyte: lymphocyte:
do profiteration: differentiation, materation, tissue damage.
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                                                                                                                                                                                                                                                                                                                                                         Hawkins PR;

    used to screen for
tissue damage associated

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RESULT W15701

132 FKLILKK 138

1 FKLILKK 7

W15701 otandard; protein,
W15701;

AΑ

Query Match
Hest Loys: Similarity
Techns 7; Conserv

Conservative

140 04: . .

Score 33; Pred. No. 2

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Mismatches

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pisclosure) Fage 22: 26pp. English.

Of the present sequence represents a novel protein from mouse liver cells. The present sequence represents a novel protein from mouse liver cells. This pictein enhances cytotoxicity of killer cells and induces their formation. It is used as an antimorbly of killer cells and induces of their formation. It is used as an antimorbly and attitudes of antihorterial agent for antihorterial agent manufacture, and in the treatment of atopic or immune system diseases, e.g. asthmus hayfever or incondition. When formationed with interleakin-3, it is also used to treat leakapenia and threetocytepaguia as conducted with control of the protect sequences. When used in attitudeour immunetherapy of leukaemia and other concers. When used in attitudeour immunetherapy this nevel protects sequences, e.g. attitudes of interleakin-2 (IT 2) compared with associated with administration of ILL2) or by addition to the patient (before administration of ILL2) or by addition to the module in which cells sequence 157 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-APR-1997.
26-SEP-1996; 305997.
20-SEP-1996; JP-269105.
26-SEP 1995; JF-270725.
29-FEB 1996; JF-067434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Movee interferon-gamma inducer protein.
Interferon-gamma, IFN-gamma; antiviral; antioncotic; radiothorapy; immuno-regulatory; and itumour apart; chemothorapy; loskopaonia; immuno-regulatory; and itumour part; chemothorapy; loskopaonia; thromboryproperate call; asthma; hayfover; thromboryproperate call; asthma; hayfover;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or treat IGIF-2 induction of proliferation, differentiation or materation of leacecytes or lymphocytes, especially in relation to tissue dament associated with inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU
Akita K, Fujii M. Kurimoto M. Nul
WPI: 97-205381/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                 immuno:competent cells - useful for adoptive immuno:therapy of
tumours and as antimicrobial agent etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                               Human protein that induces interferon-gamma production
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurimoto M. Nukada Y. Tapimoto II
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Pred. No. 2.8:
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26-JAN 1998 (first entry)

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Human priticis that is along thereby a ground in principal that is and as antimaticable agent etc.

So Claim 8: Page 202 2666. English.

CC The proper to represent a large protein from human cells, which contains the following production in immunocompetent cells that protein represent a large production in immunocompetent cells for this protein enhances systematicity of filler cells and induces their contains a subject of innoting an it-AIDS) or antitumour contains a subject of innoting anti-AIDS) or antitional agent, and in the treatment of atopic or immune system diseases, e.g. asthmatic and in the treatment of atopic or immune system diseases, e.g. asthmatic and in the treatment of atopic or immunes system diseases, e.g. asthmatic and the rest lessonal and therefore with interlepting and other cancers. When used in the formatic protein effect of interlepting significantly improves the immunotherapy of these novel protein significantly improves the containstructure of the containstructure of the contains the medium in which cells sequence 157 AA;

Sequence 157 AA;
WASSULT WASSUL
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Best Local
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26-SEP-1996.
20-SEP-1996.
20-SEP-1996.
20-SEP-1996.
26-SEF-1997.
29-FEB-1996. ID-067434
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21-MAY-1998 (first entry)
Amich anid saguerah of Euman interleubin-1-gamma.
Interleubin-1-gamma, TD-1-gamma; mouse, cytokine, IGIE; interferon-gamma;
induction schikody, diagnostic assay; fusion protoin, activity,
immunological disorder; allergy
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Interferon gamma, IPN-gamma, activital; antiongotic; radiotherapy;
immunoregulatory, antitumour agent; chemotherapy; leukopaenia;
thrombotytegachi, immunochipetest cell; astima, hayfover,
rheumatism, interleukin; killer cell
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AKIL: F. FIJILM. KILIMULL M. NIJ
WPT: 97-205981/19
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41. .47
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                                                                          108.
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Best Local
27.JUN-1997) 304616.
27.JUN-1995; JP-185305.
27.JUN-1995; JP-185305.
(HAVB ) HAYACHIBARA SELEUTSU K.
KULTIMOKO M, OKUTA T, TOTTIGOĐ K.
WPI: MARIOA4914706.
N-PSCB: V15825, V15825.
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                                                                                                                                                                                                                        Interferon-gamma production inducer
Interferon-gamma IPN-gamma, Filduction inducer, gono thriugy/
Immuno-content of 1 thestment; prevention, malignant to-curr
viral infection, Executial infection, immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antagenis' of Noman Interleable legarma (1888) for immunological disorders caused by human IL-1-gamma Disclosure: Pages 54-55; 65pp: English.
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N-PSDB: V05368.
                                                                                                                                                                                                  Key
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W47429;
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                                                                                                                         Mist_difference
                                                                                                                                                                                                                                                                               U5-JUN-1998 (first entry)
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7, Conserv
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F, Hardiman GT, Kastelein
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147. .
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Pred. No. 2.8;
Mismatthes
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                                                                                                                                                                                                                                                                                                                                                                                                                  This is an interferon quamma (IFN-gamma) inducing polypeptide sequence. This religion in threes IFN-gamma production in immunocompetent cells the polypeptide is not camed but is described in JP 27198/96 and is co-/96. As expansion example the presented form of this polypeptide but this polypeptide in the sequence of this polypeptide but this polypeptide is not obtain by closwing a linkage between Asp at amino acid possition 37 of the precursor. The entry of a few dataset to bound the precursor of the precursor 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                manner lan
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[14.2.2.1 + 14.8.3 + 50.7.74pp. English.]
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This sequence represents the precursor of an interferon-gamma (IEN-gamma) inducing polypeptide. The polypeptide induces IEN-gamma production in immunocompetent cells (the polypeptide induces IEN-gamma production into 12 27199,96 and 19209,96). An enzyme can convert this precursor form into its active form by cleaving a linkage between Asp at amino acid position 36 and Tyr at amile acid position 35 tells without the convert and can be obtained from a human harmatepointh cell and can be inhibited by induce tamile and acetyl introsyme can be used for cleaving a recombinant IEN gamma pro polypeptide to form a mature polypeptide.
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Interferon-gamma, IFN-gamma, procursor, encymes cleavage.
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A:Genome: plastid
C:Superfamily, DNA-directed SNA polymerase beta chain
C:Keywords: nucleotidy)transferase, plastid, transcri
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A;Molecule type: DNA
A;Besidues: 1-379 <ISE>
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R)Iserentant, D.; Verachtert, H.
Yeast 11, 467-473, 1995
A)Title: Cloning and seguencing of the LET2 branchague general
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A:Accession: 872282
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ArTitle: Complete gene map of the plasmid-like DNA of the mularia purasite Plasmodium
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A.) Rose of 7 Mag. B. Shao, Y.
Shirle CT, 1851162, 1997
A.Fitcle Complete genome sequence of Escherichia cell K-12
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A.Note sequence extracted from NCBI backbone (NCBIN:112737, NCBIP:112738)

A.Note gar for the sequence will separate the filler than the sequencing for the sequence of general transcription factor IFIIB and relationships to oth A.Title. Sequence of general transcription factor IFIIB and relationships to oth A.Rocession: A56407

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ArTitle: Crystal structure of a TFIIB TBP TATA element ternary complex.
ArReference number: A57980
ArContents, annotation, X-ray crystallography, 2.7 angstroms, residues 112-316
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A.Gross-references. EMBL.X51868; NID:g65128; PID:g65129
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A:Reference number: A70100; MUID:48065943
A:Accession: H70153
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p:Hisatako K : Malik, S : Pooder: 8.G.: Horikoshi, M.
Nucleic Acids Res 13. 6533, 1391
A:Title: Gonserved structural motifs between Xenopus and human
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7.Species. Burrelia bulgdorferi (Lyme disease spirochete)
7.5545 - 7.554 | 1998 | #sequence_revision 13.Feb·1998 | #text_change US Jon 1998
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C.Species. Xemopus laevis (African clawed from)
"Plato" (2:Nothing #somponne_romision "Place 1995 #fext_clumen 17-Jul-1998
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n., C.: Garland, S.: Fujii, C.: Cotton, M.D.: Horst, K.: Roberts,
aon, san-aak, 1997
5 FKLILK 10
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Com. Casjens, S.: Huang, W.M.: Sutton, G.G.: Clayton, R.: Lathiern.
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probable membrane protein VJF1260 ) bust (Saccharomyces derevisiae)
NiAlternate names: hypothetical protein J2050
C:Species. Saccharomyces derevisiae
C:Acte: 23:Aux:1393 **sequence_revisiae
C:Acte: 23:Aux:1393 **sequence_revisiae
C:Accession: S57149
R:Rose: M.: Koeter: P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56848
A:Residue: 1514
A:Residue: 151 <ROS>
A:Cross:reference: EMEL:249626: NID:g1015854, PID:g1015855; MIPS:YJR126c
C:Genetics:
A:Map position: 1CR
C:Keywords: transmembrane protein
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A.Status: preliminary
A.Molecule type. DNA
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hypothetical protein slr1066 - Symechocystis sp. (Strain PCC 6803)
Cypecies: Symechocystis sp.
Cypecies: Symechocystis sp.
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## SUMMARIES

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                                    CULHANE A.C., HALL M.D., ROTHWELL N.J., LUHESHI (). "Cluding of rat brain interleukin 18 ctNA.", MOL. PSYCH. 3:362-366(1998).
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HTPOTHETICAL 30, 1 KD PROTEIN.
BORFFELTA BURGDORFERI (LYME DISEASE SPIROCHEIE).
BACTERIA- SPIROCHAETALES: SPIROCHAETACEAE; BURKELIA.
                                                                                                                EUKARYOTA: METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
ROTENTIA, (CIUR-JUNAIHI, MURICAE, MURIMAE, KATTUS)
                                                                                                                                                                                                                                                                                                                                                                                                                SUBMITTED (JUL-1998) TO EMBL/GENBANK/DUBU DAIA HANKS EMBL: U30617; -...
HYPOTHETICAL PROTEIN.
SEQUENCE: A'S AA. COLLA MW. BUCALISE CROZE:
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"Evidence for in vivo but not in vitro expression of a Bouroila burddorferi outer surface protein F (OspF) homologue.":
MOL: MICROBIOL 18:507-520(1995).
 SECURINCE
                                                                          STRAIN-SPRAGUE DAWLEY: TISSUE-WHOLE BRAIN;
                                                                                      SEQUENCE FROM N.A.
                                                                                                                                         RATTUS NORVEGICUS (RAT)
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 194 M
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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 22913 MW;
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Pred. No. 47:
2: Mismatches
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            POTENTIAL
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RESULT
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Best Local Similarity
5: Conserv
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Match.
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J. INFECT. DIS 0.0-0(1008)
EMBL; AFC20027; 32657921; -.

NON_TER 1 1

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NON_TER 551 AA: K147K MW.
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O55346:
O1-JUN-1998 (TREMBLEFT O6, CPEATED)
O1-JUN-1998 (TREMBLEFT O6, LAST SECRENCE UPDATE)
O1-TUN-1998 (TREMBLEFT O6, LAST ANNOTATION UPDATE)
GLYCOPROTEIN G1 AND G2 PREDURSOR.
                                                                                                                                                                                                                                                                                                                                          LEVIS & MORTHNOV S TO POWE SABATINE M. ST JECK S.C.);

J. INFECT. DIS 0.0-0(1998).

EMBL: AF028024; C2653915; -..

SECUENCE 1138 AA. 127548 MW.
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01-JUN-1998 (TREMBLREL 05, CREATED)
01-JUN-1998 (TREMBIREL 05, LAST SECTENCE UP
01-JUN-1998 (TREMBIRET 05, LAST SECTENCE UP
01-JUN-1998 (TREMBIRET 05, LAST ANNOTATION OF
CLYCOPROTEIN OF AND 02 PRECURSOR (FRAGMENT).
MACIEL VIRUS.
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  055349
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05, LAST SEQUENCE UPDATE)
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RESULT 10
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AC Q26049
PT 01-MOV
DT 01-MOV
DT 01-MOV
DT 01-MOV
DT CELL S
GN BEP3.
GN BE
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C STRAIN-SKORN:

(X MEDLINE: 92374987.

(A NEUVILLE P., AIGLE M.:

"Ore2, a mutation affecting proline biosynthesis in the year

EX Saccharomyces occavision, loads to a edo phonotype.";

PI MOL GEN. GENEI. 274:192-200(1994).

CR EMBL; X57338; G434969; -.

MON TER 1 1 1

MON TER 175 AA: 29868 MW: L3AFYEAB CFC72:
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01-JUN 1998 (TREMBLEEL,
03-JUN-1998 (THEMBLEEL,
GLYCOPHOJEIN G1 AND G2 P
PERGAMINO VIRUS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
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01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
101-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
101-NOV-1996 (TREMBLEEL 01, CREATED ANNOTATION UPDATE)
0RE2 DELTAT, PYSEGLINE 5-CARROXYLATE REDUCTASE (FRAJMENT).
SACCHAPOMYCES CEPEVISIAE (BAKEP'S YEAST).
SACCHAPOMYCES, SACCHAROMYCETALES:
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206790;
PARACENTROTUS LIVIDUS (COMMON SEA UECHIN).
EURARYOTA, METACOA, ECHINICEEMATA, ECHINICIA:
ECHINATEA; ECHINICIPA; ECHINIDAE; PARACENIMOTU
                                                                                                                                                                                              CELL SURFACE PROTEIN BEP3.
                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TREMENTED OF OLONO - 109 (TREMENTED OLONO - 109 OLONO
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J INFECT DIS (0.0-0(1448)).
EMBL: AF028028; G2552923; -..
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M. PEILMERE B., COCALLAGIAN M., PARSONS J., PERCY C.,
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RESULT 13
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DEAP S. DOT Z. DOTREN N. P. PARFICIA N. PULTON
HAWKINS T., HILLIER L., JIER M., JOHNSTON L., JONES N., KENSHAW J.
KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
MCMURRAY A., MORTIMORE B., O'CCALLAGHAN M., PARSONS J., PERCY T.
MCMURRAY A., MORTIMORE B., O'CCALLAGHAN M., PARSONS J., PERCY T.
MILKEN L., POOPEA A., SAUNDERS D. SHOWNKEEN F. SWALDON N., SMITH
SONNHAMMER E., STADEN P., SULSTON J., THIEREY MIEG J., IHOMAS K.,
WILKINSON SERBOAT J. WOHLDMAN P.
SIGNAL
SIGNAL
                                                  -1- SIMILARITY: HIGH, TO OTHER PLANT PEROXIDASES EMBL; L13654; G678547; -. PFAM: PF00141: peroxidase; 1.
                                                                                                            BOTELLA M.A., QUESAIA M.A., HASBGAWA P.M., VALPUESTA V.;
"Nurleotide sequences of two peroxidase genes from tomato
(Lycopersicon esculentum).";
PLANT PHYSIOL. 103 ±63 ±64 (1993).
-1- FUNCTION: FEMOVAL OF H(2)°(2), CXIDATION OF TOXIC MEDUCHANIS,
BIOSYNTHESIS AND DEGRADATION OF LIGNIN, DEFENCE RESPONSE TOWARD
WOUNDING AND METABOLISM OF AUXIN. THESE FUNCTIONS MIGHT BE
DEPENDENT ON EACH ISOZYME/ISOFORM IN EACH PLANT TISSUE.
-1- COTALYTIC ACTIVITY DONOF: H(2)°(2) CXIDIBEE CONE 2 3(2)**
-1- COPACTOR: THIS PROTEIN BINDS HEME.
                                                                                                                                                                                                                                                                                                                                                                            INT FERSION ESCULENTUM (TOMATO)
EUKARYOTA: VIRIUFLANIAE: CHAMOPHYTA/EMBRYOFHYIA: GECOT: EMBROCHYTA:
TRACHEOPHYTA; EURYPLLOPHYTES: SEPRMATOPHYTA: MAINOLTOPHYTA:
EUROFCOTYLFEONS: ASTERITAE: SOLANANAE: SOLANALES: SOLANACEAE: SOLANANO
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01-NOV-1996 (TREMBEREL 01. LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBEREL 02. LAST ANNOTATION OFFAT
PEPOXIDASE 1 PRECUESOR (EC 1.11.1.7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q07446;
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01-NOV-1998 (TREMBLREL 08, LAST SEQUENCE UPDATE)
01 NOV-1998 (TREMBLREL 06, LAST ANNOTATION OF DATE)
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EMBL: Z66563; E1322451;
SEQUENCE 2610 AA; <2
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EUKARYOTA; METAZOA; NEMATODA;
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                                 POREDULIASE: GLYCOPROIEIN: PERGXIDASE; HEME:
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PRELIMINARY: PRI: 401 AA. P72902
01-FEB-1997 (THEMBLREL 02. CREATED)
01-FEB-1997 (TREMBLREL 02. LASI SEQUENCE UP
01-NOV 1998 (TREMBLREL 08. LASI ANNOTATION
HYPOTHETICAL 46.0 KD PROTEIN.
SYNECHOCYSIIS SP. (STRAIN PCC 5803).
SYNECHOCYSIIS SP. (STRAIN PCC 5803).
                                                                                                                                                                                                                                                                   EU ARABIDOPSIS SEQUENCING PROJECT;
SHEMITTED (1871-1948) TO EMBL/ARNHANK/HARJ DATA BANKS
EMBL: ALO31032; E1310395; -.
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01-NOV-1998 (IREMBLREL, 08, LASI SEQUENCE UPDATE)
01-NOV-1998 (TREMBLEEL OR, LAST ANNOTATION UPDATE)
HYPOTHELICAL 36.1 KD PROTEIN.
E1715.120.
 SEQUENCE FROM N.A. TABATA S.;
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                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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EUKABIDTA VIBIDIBLANTAR, CHARGHYTA/EMMRYGEHYTA GRGUP;
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Similarity 71.4%;
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IS; ROSIDAE; CAPPAPALES; RFASSICACEAE; APABIDOPSIS
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PPOXIMAL HISTIDINE (HEME AXIAL LIGAND)
(BY SIMILARITY.
BY SIMILARITY.
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Pred. No. lc+02;
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MEDIZINE: 97051201.
FANEFO T SATO S FOTANI H IANAFA A SARATTU F. MAY
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MOTANTA T MATENIA A MOTANIA T WATANABE A., YAMADA M.
                                                                                                                                                                                                      Synechocystis sp strain PCC6803. II. Sequence determination of the cutire Jenome and assignment of potential protein coding realons. DNA RES. 3:109-136(1996).
EMBL: D90901: G1651992: -.
DPAM: PF00534: G1ycos_transf_1: 1.
HYPOTHETICAL PROTEIN.
EMPLOYED AND AND AND MAN. BUDGLEGGS:
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TABATA S.;
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71.4*;
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Gepyright (c) 1993 - 1998 Gompugen Ltd
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RESULT
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AC R9
DT 29
DT HL
KW TF
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COS HC
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DR N.ESSA. 192506.

PT Protein that induces games interferen products limitation potent profils used a graph satisfact and the most agent also induces profils. Used a graph and interferent agent also induces profils. Sequence represents the interferent jamma (IENJamma) induces profils sequence to this protein is useful as an antiviral, of the invention in this protein is useful as an antiviral, and thomost, artisepile, immunocompetent cells. The protein is useful as an antiviral, and the most force of the invention in the protein of immunocompetent cells. The protein is useful as an antiviral, and the new force of invention of artisepile, immunocompetent cells. The protein or preventing AIDS, condylona dominatum, of indices of fermion or protein can also be used to induce IPNAMMA production in the cells and when used with intersection in the protein can also be used to induce IPNAMMA production in the cells and when used with intersection in the cells and the cells are incompeted with intersection in the cells and the cells are incompeted and the cells are produced and intersection in the cells and the cells are incompeted and interest of the cells and the cells. The branch is sequence can be used to induce the protein assayed, sequence 157 AA:
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Interferen gamma freduction inducer protein.
Interferen gamma; inducer; IFNgamma; immunocompetent call; antiviral;
antitumour; antiseptic; immunoregulatory; platelet increasing agent;
therapy; prevention, condyloma adumination, recal cancer; brain cancer;
granuloma; mycosis funcoides, rheumatism; allergy; cytotoxicity; AIDS;
Liller Toull interfeuelling; conceinnal antibody.

Mus musculus.
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Human interferon-gamma inducer protein.
Interferon-gamma inducer protein: TEN-gamma, antivira antitumbur, antibacterial, immunoregulator, adoptive
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13-JUL-1995, 304906.
14-JUL-1994, JP-184162.
10-FEB-1995, JP-045057.
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                                               therapy: cancer.
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Kohno K, Kunikata T, Kurimoto M, Okamura
                                                                                                                                                                               k99564 standard; Protein; 157
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WFT, 96:079377/08.
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  Location/Qualifiers
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100.0%; Fred. No. 16;
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"When the different damma producing polypeptide - the real present each viral disease, malignancies and
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S, Keimo E. Ferikata T. Eurimoto M,
hi W. Landeveto T. Toridoe K, Ushio S.
             ise 4 44pp; English.

he is problem (Reebbe) induces interferon gamma (IEN gamma)

y " do emperent cells. It enhances the cytotoxicity of
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Pred. No. 15:
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R99560

R99560; 29-SEP-1996

(first entry)

R99560 standard; Protein; 193

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Best Local Similarity 100.0%:
Matches 5: Conservative 0
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15-NOV-1994; JP-30A203.
23-FEB-1995; JP-058240.
10-MAR-1995; JP-078357.
18-SEP-1995; JP-26262.
29-SEP-1995; JP-274988.
                                                                                                                                                                                                                                                                                                                                                           Fukuda S. Kohno K. nu.....
Taniquchi M. Tanimoto T. Torigoo K.
Whi: 96-150837/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic Trecils). Recombinant IFN gamma inducet protein can be produced in high yields using host cells, esp. Escherichia coli, transformed with a wester carrying the enceding cDNA (T32402). It is useful as an antiviral, antitumor, antibacterial, immunorogulatory and blood platelet enhancing agent, and can be used in adoptive immunotherapy. It is also used to raise monoclonal antibodies. A full-length sequence is given in R99560.
                                                                                                                                                                                       A novel mouse protein (R9959) induces interferon-gamma (JEN-gamma) prodn. by immunocompetent cells. Its sequence was deduced from that of a cDNA clone (T32403) isolated from a mouse liver library. Recombinant IFN-gamma inducer protein can be profuced in high yields using host oralls, esp. Fschorichia coli, transformed with a rector carriers.
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                                                                                                                                                                             carrying the cDNA.
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                                                                                                                                                                                                                                                                                                          disorders
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Fukuda S, Kohno K, Kunikata T, K
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Zative 0: Mismatches
                                                                Score 27; DB 1; Length 157; Pred. No. 16; ; Mismatches 0; Indels
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30-NOV-1994.
18-FFR-1994.
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10-MAR-1995, JP-078857

18-SEP 1995, JP-078857

29-SEP 1995, JP-274388

(HAYE) HAYASHIPANA SEIRHTSU KAYAKU,

PUKUJA S. PROBLEM F. PURUJA T. KUTIMCCO M,

Taniquohi M. Tanimchu T. Tuliguu K. Ushio S.

WPI-06625197779
Model for screening upds, for inhibition of recombinate test transformed with gene for ATPase under cortrol of induncible promoter Disclosure, Fld 2, Tap. German.
Helicobacter specific Almase genes 439, The
                                                                            Melchers K, Schaf
WPT: 96-286831,799
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Helioobaoter pylori; ATPase; model; screening: metabolism
Helioobaoter pylori
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Sequence 193 AA;
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Claim 6; Page 41-42;
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RESULT W06103

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MR3 Winters (WSC02) is a fusion protein composed of bushan syelin basic protein (MRP) foetal isoform MRP21.5 (see also W00296) and delta PIPA (W00400), a proteclipid protein (PEP) matein that lacks hydrophobic domains 1.3 and 4 of native human PLP (W06106) but includes PLP aptropes associated with multiple sciences (MS). It can be expressed in a coll transformants using a DNA construct (T4182) world. The MR21 will be seen fisher M23 while the map of the Can be expressed in a coll transformants will a DNA construct (T4182) world. The MR21 is delta ELP3 game fisher M23 while the M21 will be seen useful for the clinical assessment, diagnosis and treatment are useful for the clinical assessment, diagnosis and treatment
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WPI; yb-
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MP3 chimwr: (MEP21 % delta PEP3 fusion).
MP4 chimwr: (MEP21 % delta PEP3 myelin basic protein, MEP;
Protectipid protein, PEE, delta PEP2 myelin basic protein, MEP;
MP521.5 multiple sclerosis, autoimmune disease; diagnosis;
MP521.5 multiple sclerosis, autoimmune disease; diagnosis;
therap; Telymphewyw. Tevil, incray; apoptosis, MP3 chimera.
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Sequence 686 AA:
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02-MAY-1995; US-431644
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Find protein: PEP delta PEP3 myelin basic protein: MBP;

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[findshowyte, firell, andray, apoptosis, MP3 chimetal.
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07-NOV-1996.
22-APR-1996: U05611.
02-MAY-1995: US-431648.
02-MAY-1995: US-431644.
07-JUN-1995: US-482114.
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MM4 chimera (WÜNIDS) is a fusion protein composed of human myolin busic protein (MBP) foetal isofouth MBP21.5 (see also WD0399) and delta PLP4 (WO6101) a proteinigh protein (PLP) mutain that larks all 4 hydrophobic domains of native human PLP (WÖ6105) but includes PLP epitopes associated with multiple solor sis (M5). It can be expressed in E roll transformants using a NNA construct (T1893) coutq, the MBP21.5 delta FLP4 were fusion. MP4 chicora and other size in the MBP21.5 delta FLP4 were fusion. MP4 chicora are useful for the clinical assessment, diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1997 (first entry)

DM4 Chimera (delta PLP4-MBP21.5 fusion).

Proteolipid protein; PLP, delta PLP4, myelin basic protein; ME8:
MBP21.5; multiple sclerosis; autoimmune disease: diagrass;
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(USSH.) US DEPT HEALTH & HUMAN SERVICES.
Lenardo MJ. Matis L. McFarland HF. Mueller
Nye SH. Pelfrey CM. Squinto SP. Wilkins JA:
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/bote= "encephalitogenic epitope in mouse model"
292. .304
/label= Epitope
/mote= "PLP =pitop=
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/note= "hexa-histidine tag facilitates recombinate
protein purification"
                                                                                                                                                            /label= Epitope
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/bote= "encephalitogenic epitope in
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(M05101) and MB215 (M0399). Delta PLP4 is a proteolipid protein (M05101) and MB215 (M0399). Delta PLP4 is a proteolipid protein (PLP) mutch that lacks all 4 hydrophobic domains of native human PLP (M05106) but includes PLP epitopes associated with muttiple sclorests (MS). MP01 is a froctal inform of human myolib basic fittels (MS). MP01 is a froctal inform of human myolib basic fittels (MS). MP01 is a froctal inform of human myolib basic state (MS). M05103). It can be expressed in bacterial bat sclls using a lNA construct (M1894). PLP polypeptides (see also W0440), Wollin on and World') van tersend in the collicial assessment, diagnosis and treatment of MS.
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Fiotoclipid protein, FLF, delta FLF4, myelin basic protein;
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07-NOV-1946: U05611.

22 AFR 1996: U5-431648.

02-MAY-1995: US-431648.

02-MAY:1995: US-431644.

07-JUN-1995: US-482114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1, Page 79-80, 156pp; English.

The notive human 21.5 \( \text{Teathel} \) issuing (\text{W0033+}) of modific basis protein, \( \text{MEP+XZCy88} \), includes an exch 2 encode; region (\text{X2}) that may contain an epitope involved in the pathogenesis of multiple solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}), the X2 region is not found in the MEP of healthy solerosis (\text{MS}) and \( \text{MS}) and \( 
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Hymnn myelin basin Fritch (foetal isoform).
Myelin basin Fertin MBP MRP-X20y-81, Frateul.pld protein: Fill:
multiple sclerosis; autoimmune disease; diagnosis: thorapy:
T-lymphocyte; T-cell: anergy: apoptosis.
                                                                         Foetal myelin basic protein MBP-M20y881/bact.
Myelin basic protein, MBP, MBP-M20y881, proteolipid protein;
multiple solerosis; autoimmine disease; diagnosis; therapy;
Trlymphocyte: Treell; ancray; apoptosis.
                                                    Synthetic.
                                                                                                                                                                                            01-FEB-1997 (first entry)
                                                                                                                                                                                                                      W06107;
                                                                                                                                                                                                                                              W06107 Standard, Protein, 203 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Threells for responsiveness to MBP epitopes and can be used as therapeutic agents that act by inducing Total responses, including anergy and apoptosis, as a means of treating MS. Sequence 197 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      scierosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human Ayelin basic protein and proteolipid protein variant(s) ased in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB: T41889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lenardo MJ, Matis I
Nyo SH, Polfrey CM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ALEX-) ALEXION PHARM INC
(USSH ) US DEPT HEALTH & I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
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01-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W00399 standard: Protein; 197
region
                                                                                                                                                                                                                                                                                                                                                                                                 84 MYKDS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 MYKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MYKDS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US DEPT HEALTH & HUMAN SERVICES MJ, Matis L, McFarland HF, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid, esp. an uncharged amino acid of mol wt below below about 15% partic. Ser, in constructs of the invention"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ∕mote= "exon 2-encoded region"
81
Location/Qualifiers
60. .85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label≃ x2
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60. .85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27: DB
Pred. No. 21;
0: Mismatches
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W09634522-A1.

PD 07-NOV-1996.

PF 22-APR-1996; U05611.

PF 02-MAY-1995; US-431644.

PR 07-MAY-1995; US-431644.

PR 07-UN-1995; US-431644.

PA (ALEX-) ALFXION PHAPM INC

PA (ALEX-) ALFXION PHAPM INC

PA (GISSH ) US DEPT HEALTH & HUMAN SEPVICES.

"SH, Felfitty CM, Squinto SE, Mulkins JA;

"SH, Felfitty CM, Squinto SE, Wilkins JA;
                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Matth 1999
Best Local Similarity 100
Matches 5 Observative
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07-W201966

22-App-1966 U25611

02-MAY 1966 U5-431644

02-MAY 1995 U5-431644

07-JUN 1995 U5-431644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A 21.5 kDa foetal isoform (W06107) of myelin basic protein, MEP+X2*ys%1/bect, is the product of a ENA construct (T41846) based on the human foetal MBP+X2*ys81 isoform (W0399) but utilising bacterially-preferred codons in place of the mative human codons (see also T41889). This increases produce the MBP in E. coli by at least for. Recombinant MBP 21.5 polypeptides (see also W00494 and W06108) are useful in the clinical assessment, diagnosis and treatment of MS.
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
Poy
region
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fratal mystic basis protoin MRF-X2Sex91/bast.
Wyells Easts protoit. XEP: MRF-X2Sex91: protoilipid protein;
multiple sclerosis; autoimmune disease; diagnosis; therapy;
T-lymphrits. T-roll, prorgy, profits(s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W06108 standard: Protein: 203 AA W0610A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALEX ARXING HAARKINI
(OSSH) OS OPT FEALTH & HOMAN SERVICES
(COSSH) OS OPT FEALTH & HOMAN SERVICES
(COSSH) MI MALIS L. MCFAILAIN HE, MU
NYE SH, Pelfrey CM, Squinto SP, Wilkin
WFI: 96-505698/50
N+FSCP: 141806/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human myelin basic protoin and protoclipid protoin variant(s) used in the assessment, diagnosis and treatment of multiple
                                                 New human myelin basic protein and proteolipid protein variant(s) used in the assessment, diagnosis and treatment of multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                     60. .85
/Tubele N2
/hote- "exon 2-encoded region, with
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                                                                                                                                                                                                                                                                                                                                                  mutation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 27, DB
Pred. No. 21;
Nismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wilkins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 200
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                                                                                                                               Mueller
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RESULT
W24262
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W24258
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SERVEDE
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Best Local 
Matches
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Best Local Similarity
Matches 5, Conserv
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17-JUN 1997
24-JUN 1996; 028722.
04-OCT 1995; JP-279906.
10-MAP-1995; JP-078357.
29-SEP-1995; JP-274998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; T80210.
N-PSDB; T80210.
A drug containing a polypeptide which induces inte-
useful for treating e.g. malignant tumours, viral,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Elseissure: Page 82:82: 155pg, English.
A 215 kDa feetal Issier (W05108) of myells basic fritoin, MBF-KISer3, bact., is the product of a DAA obstituat (1:337) based on the human feetal MBP-KICY881 issform (W00399) but utilising codons that are highly expressed in bacterial genes in place of the native codons (see also 741889) and incorporating a sequence coding for a hexa-histidine tail. This allows large-scale produced and purification of the MBP in bacterial basis. Focumbinant KBF 215 polypeguides (see also W0544 and ku2127) are useful in the originical assessment, diagnosis and treatment of MS.
          15-007-1997 (first entry)
Human protein for induction of interferon-gamma.
Interferon-gamma; immunocompetent cell; malignant tumour;
Viral disease; banterial infection, immune disease.
Homo sactors
                                                                                                                                                  W24258 standard; Protein; 157 W24258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence impresents a protein which induces interferon-damma production in immunicarpoint talls. This protein and tracked as the major component in a drug for the prevention and tracked to a garalignant turnours, which diseases, bacterial infections and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine protein for induction of interferon-gamma.
Interferon-gamma, immunocompetent cell, malignant tumour:
Vital disease: bacturial infection; immuno disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W24262;
15-00T-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure, Fage 10-11, 12pp.
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97-4594/91/34.
sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diseases.
ce 157 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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100 0*;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Store 27; ()B
Pred No 16;
() Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein a protein search asing sw model
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arcater than or equal to the score of the result being printed,
a derived by analysis of the total score distribution.
              US-09-030-061-4
27
1 MYKDS 5
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Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR_58:*
1: pir1:
2: pir2:
3: pir3:
4: pir4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 50000000
2 50000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116738 segs, 37460341 residues
           Copyright (n) 1993 - 1998 Compugen Etd
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        ם בו
נייוטן לה השתונים ממת ממת מת מת מת ביינוט ביינוט ביינוט ביים המת ביים
מינוט המת מת מת מת מת מת מת מת מת ביינוט ביינוט
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A, Fesidoes 1:197 : FE3:
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Chem. 259, 5028 5031,
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RiBoylan, K.B.; Ayres, T.M.; Popko, B.; Takahashi, N.; Hood, L.B.; Prusinot. Genomics 6, 16-22, 1940
A.Tillo Pepcitive DNA (700A)s 5, to the human myelin hand, pistile account AReterence number: 154219; MGID:90152679
A:Stalus - 0-17-7
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A. Tille Evidence for the expression of four myella basis A. Reference number: 156567; MUID: 87311781
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A:Residues: 20:25 (X),27:29 RBCD
2.29mmept. Four alternatively spiloud form
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Arch. Blochem. Blophys. 200, 174–180, 1995
A;Title: The isolation and characterization of four myelim basic proteins from
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A:Tittle: Isolation and patrial characterization of mothylated arginines A:Reference number: A90252 MUID:7266401
A:Reference number: A90252 MUID:7266401
A:Contents: annotation: methylarginine
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J. Biol. Chem. 264, 5121-5127, 1989
A.Title. The isolation, characterization.
A:Reference number: A33273: MUID:89174797
A:Accession: A33273
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R.F.th, H J , Frengalst, M., Pieterius, P.J., Ciandall, B.L., Campasholl,
J. Neurosci. Res. 16, 227-238, 1986
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A;Reference number: A92806; MUID:71088405
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golli-myelin basic protein precursor - mouse
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N.Contains: myelin basic protein
C.Specles: Mus musculus (bouse mouse)
C.Specles: Mus musculus (bouse mouse)
C.Str. 17-8: 1387 #88798905_F871Sion 67 "cot.1894 #text_change 20-F85-1998
C.Achersi: A47421 #45421_A08878_A92867 - A28691 #F28591 A68620, 148497
R.Campagnord A.T. F87671 T.M. Campagnoni, C.W., Kampf, K., Amur Umarjee,
J. Biol. Chem. 278 4220-4228, 193
A.Title: Structure and developmental regulation of Golli-mbp, a 105-kilobase
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AsResidues 194:074,016:329 (MEWI)
AsCross-references GR M15060; NID
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A:Moleculo type: mRW
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A.Molecule type: mR
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Experimental source. Sloke M722, Accession: B26591
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A;Rosidoes: 134-157 AMID>
A;Rosidoes: 151-156, Milra, M., Acyama, A., Tecroba, F., Or Rembo J. 7, 77-83, 1988
A;Title: Gene organization and transcription of deplicated MBC A:Fortune organization and transcription of deplicated MBC A:Fortune organization (151256; Multi-AA14604
A;Accossion: 153256
A;Status translatio: T. & W. Translation for Te,EMBJ,CDBJ
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Areasibuss: 1-191. (SREF)
Arcross-references: EMBLIX67319; NID:q51332: PID:q51333
Arcross-references: EMBLIX67319; NID:q51332: PID:q51333
Arcross-references: EMBLIX67319; NID:q51332: PID:q51333
Arcross-referenced to the EMPLIData Library, July 1992
Bricollor, W.K.: Hunkeler, M.J.: Campagnoni, A.T.: Sprague, J.: Lazzarini, R.A.:
Proc. Natl. Acad. Sol. U.S.A. 81: 18-22; 1984
A.Fithe Characterization of mouse myolin busic procession: IS8996
A.Fofencies number: ISE/MY: MUIT:34119431
A.Accession: IS8996
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A.Experimental source M41 splice form 14K
A.Experimental source M41 splice form 14K
T. Neurochem. 59, 2318 2327, 1992
Arfitle: A novel transcript overlapping the myelin basic protein
A.Reference number: 148407; MUID: 93057597
A.A.Accession: 148407
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A.Hesilbes: 117-229; PAN, 123-250 300A;
A.Hesilbes: 127-229; PAN, 123-250, PAN, 123-250
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A.T. The promoter elements of the mouse myelin basic protein dend fun. A.Feference number. 154-72, MUICLES.51919
A.Accession. 154-033
A.Starts profilming Tracelored from 35, EMEC, DDBC
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A:Molecule type: mRNA
A:Pesidos; 219-248 (ZEL)
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A:Status: preliminary: translated from GB/EMBL/TOBU
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Schen (13, 73, 75, 1 or)
ArTitoe Artivation of mouse Tobelpor orlis induces abundant preproeskephalis mRNA systi
ArRefore combon: A47580
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A Experienta ta sur telskitalis H31
Frances (July 1812 Solutions) Silabitwyler Ridi, Soderberg, C.; Lahesmaa, R.; E
Infort (Jemun 5), 174, 4714, 1902
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G.: 314-8714, 1992
(5) (1) In (K. and arpE homologues from Borrelia burgderteri and comp
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A:Molecule type: DNA A:Residues: 1-743 - VVAN> A:Gross references. EMBL.CD9212, NII A:Experimental source: strain S288C

NID.9486536, 115.44865

A;Reference number: \$38130 A;Accession: \$38143

Rivan Vliet Reedlijk, J.C.; Planta, R.J. submitted to the Protein Sequence Database, March 1994

hypothetical protein MRIGHTW lomolog YEESTTW yeast (saccharons) es cerevisiae)

C: Accession:

S38143

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C:Accession: 664618

R:Tomb, J.F.; White, O.; Kerlavage, A.R.: Clayton, S.A.: Sutton, G.O.: Sicksolmann, R. R:Tomb, J.F.; White, O.; Kerlavage, A.R.: Clayton, S.A.: Sutton, G.O.: Sicksolmann, R. Peterson, S., Loftus, R. Richardson, D.; Bulson, E.; Khalak, H.C.: Clove, A. Moroson, J.D.: Kelley, J.M.: Cotton, M.D.: Weidman, J.M.: Fujii, O.: Bowman, C. Weithey, Nature 388, 539-547, 1997

A:Anthers: Hayes, W.S.: Rorgovsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.C.: Evasor, C.M.: Vento, A.; Reference complete growsky, M.; Karpk, D.S.: Smith, H.S.: Smit
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R:Wallich, R.; Helmes, C.; Kramer, M.D.; Simon, M.M.
submitted to the EMBL Data Library, August 1992
A:Pescription: Characterization of an HSP70 related protein transference number: 825155
A:Accession, 825155
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Atresidues: 1-686 <TOM>
Atresidues: 1-686 <TOM>
Approximation of Architectide binding domain homology

Elsen-dagle-dagle dagle-dagle-dide binding domain homology
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A; Bosidues: 1-635 <WAL>
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A: Residues: 1-635 <TIL>
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A:Residues: 1-686 <TC
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hes 5; Conservativo 0; Mismatchor
1 MYKDS 5
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Gracession, S07383
R.Ragheb, J.A.: Dottin, R.P.
Winleig Ards Est, 15, 1891-1906, 1987
ArTitle: Structure and sequence of a UCF glucose pyrophosphorylase gene of Dictyostellum
ArReterance number: S07383; MOID:87251075
ArAccession: S07383
                                                                                                                                                                     A:Molecule type: DNA
A:Residues: 1-511 <RAG>
A:Gross references: EMML:Y00145; NID:q7384; PID:q7385
G:Gomment: This enzyme catalyses alpha-D glucose-1-pha
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ArMap position: 11s
OrKeywords: transment:and
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A:Mologile rupe: mRNA
A:Pesidons: 1:102 - 008A
A:Crose:reference: ENB! 540040
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RESULT
                                                                                      Ouery Match
Best [003] Similarity
1-50g 4: Conserv
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Matches 5: Conservative 5
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Search completed: June 22, 1999, 10:58:48 Job time: 147 sec

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REMUTPHY, L.: Niblett, D.: Harris, D. sukmitted to the EMBL Data Library, November 1995 A:Reference number: 862573
A.Accession, 362577
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A.Map position: 11p15.5-11p15.4
C:Superfamily: herpesvirus ribonucleoside-diphosphare reductuse lurge chili.
C:Keywords: DNA replication, oxidoreductuse
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                                                                                                                                                     A:Introns: 7/1
C.Superfamily, herpesvirus fiberorlesside-diphosphato reductase large chain
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Best Local Similarity 80.0%;
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INFECT. IMMUN. 60.070
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-!- FUNCTION: ACIS AS A CHAPPEONE (BY -!- INDUCTION: BY HEAT SHOCK.
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Best Local Similarity 100.0%;
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EMBL: U90434;
MIM: 600953;
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CONFLICT
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CONTT R , KIM S J. TIMIL C., CHUN H.S., JOH T.H.;

SUBMITTED (FEB-1997) TO EMBLICATENBANK/FORDI EATA FANKS.

-1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPIN-
AND STIMULATES INTERFEREN GAMMA PROOUCTION IN THELPER
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15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
16THEREBUKIN-18 PACTOR) (INTEPLETIKIN-1 GAMMA) (IL-1 SAMMA).
16THEREBUKIN-19 GAMMA) (IL-1 SAMMA).
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EUKARYOTA, METACOA, (
EITHERIA, FRIMATES.
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PHOSPHORYLATION (PUBARLE).

E -> K (IN REF. 1).

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DT 15-UUL-1998 (REL. 36, CREATED)

DT 15-UUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

DI 15-UUL-1998 (REL. 36, LAST ANNOTATION UPDATE)

DE INTERLEUKIN-18 PRECUESTE (TI: 5) (INTERFERON-SAMMA INCOCING FACTOR)

DE (IFW-GARMA-INCOCING FACTOR) (INTERFERON-GARMA) (IL-1 GARMA)

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MEDLINE: 97174446.
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EUTHERIA: RODENTTA.
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15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
101-1998 (REL. 36, LAST ANNOTATION UPDATE)
111-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
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- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND SIMULATES INTERFEHON GAMMA PROCUCTION IN THELPER TYPE I
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Pred. No. 8.9;
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Best Local Similarity

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Best Local Similarity 100

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PY7636; P97637;

15-JUL-1998 (REL. 36, CREATED)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)

INTERLEMENT-18 PRECUPSOR (TL-18) (INTERLEMENT-CAMMA INDUCING FACTOR)
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SUBMIFIED (JUL-1997) TO EMEL/GENEANK/DUEJ DATA BANKS.
-!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS AND STIMULATES INTERFERON GAMMA PRODUCTION IN THELPER TYPE I
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1 HEGE CHEM. LTLICAGE LOGG. (1997).
1 FUNCTION ANGENES MATGRAY KHILES CRIL ACTIVITY
AND STIMULATES INTERFERON GAMMA PRODUCTION IN T
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VER PRODUCTS: HUMANS HAVE THERE FORMS ARE P.

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G. (3/11) (B.3-Δ) (33-43-62-43-66 (13-85))
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                                                                                                                                                                                                                                                                                                                                                                                 CNLLITE:
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                                                                                                                                                                                           LOS NEED WEEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND 14 *-146 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. (F. (1786)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE TENTE
ACETYLATION (MONO::5% OR DI::50%)
                                                                                                                                                                                                                                                                                                                                                                                                    THREE FORMS ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N.A
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MBP_MOUSE
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Best Local Similarity
5: Consort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARSPLIC
SEQUENCE
                                                                                                                                       -11 SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYHLIN.
-13 ALTERNATIVE PRODUCTS: MCUSE HAS FOUR FORMS OF MAP, 21.5KN
-17KD, AND 14KD, FRESENI IN RELATIVE AMOUNTS OF 1:10:3.5:35.
-14 FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
-15 THE SEQUENCE SHOWN IS THAT OF THE 21.5KD FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OI-JAN-1984 (REL UB. LAST OI-UCT-1996 (REL 34, LAST AMYELIN BASIC PROTEIN (MBP).
                                                                                                                                                                                                                    MIURA M., TAMURA T. GENE 75:31-38(1989)
                                                                                                                                                                                                                                                                                                                               TAKAHASHI N., ROACH A..
CELL 42:139-148(1985).
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (18.5 KD FORM). MEDLINE; 85254913.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ALL FOUR FORMS). MEDLINE; 86079555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P04370;
20-MAR-1987 (REL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                     SEQUENCE OF 1-23 FROM N.A.
                                                                                                                                                                                                                                                                                    NEWMAN S
                                                                                                                                                                                                                                                                                              MEDI.INE; 87118269
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (17
                                                                                                                                                                                                                                                                                                                                                                                                LAZZARINI R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                        DE FERRA F., ENGH H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBP_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYKDS
                                                                                                                                                                                              FUNCTION: THIS PROTEIN MAY FUNCTION TO MAINTAIN \text{PK} \cdot \text{PER} OF MYELIN.
     M11533 G387414
M11529 G387714
M11529 G387714
M11530 G387714
M11531 G387714
M11533 G387715
M11533 G387715
M11539 G387715
M11539 G387715
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M11539 G387715
M11539 G387715
                                                                                                                                                                                                                             89252919.
.. TAMURA T.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RODENTIA
                                                                                                                                                                                                                                                                                     KITAMURA K
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196 /
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                                                                                                                                                                                                                                                                           ACAD.
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                                                                                                                                                                                                                                                                                                                                                                                     727(1985).
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G387415;
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OB. LAST SEQUENCE OFFIAIF;
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JOINED
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JOINED
                                                                                                                                                                                                                                                                                                          KD FORM).
                   JOINED
                                                                        JOINED
                                                                                                                                                                                                                                                                       CAMPAGNONI A.T.;
U.S.A. 84:886-890
                                                                                                                                                                                                                                                                                                                                          TEPLOW D.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Σ
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: 0A8864EE CRC32;
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MISSING (IN 18.5 KD FORM AND 17.2
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                                                                                                                                                                                                                                                                         84:886-890(1987)
                                                                                                                                                                                                                                                                                                                                          PRUSINER
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### PATENT AND THE PA
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SEQUENCE OF 29
TISSUE=T-CELL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P22005;
01-AUG-1991 (REL. 19, CREATED)
01-AUG-1991 (REL. 19, LAST SECURENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
FROENKETEALLY A FRECURSOR.
    MEDLINE: 86179902.
TTPAMSKI G PENET
LEE F.D.;
                                                                                                                                                                                                                            MEDLINE: 90287163.
KIIPATPICK D.L. ZINN S.A., FITZGER, MEYERHARDI J.;
MOY CELL BIOL 10:3717-3726(1990)
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUSCULUS (MOUSE).
EUKARYOTA: METAZOA; CHORDATA.
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P22005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUTHERIA PODENTIA.
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RESULT 11
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Best Local S
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CONSTRUCT
CONSTRU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENK_KAT SIANDAND; PRT; 269 AA P04094; 01-NOV-1986 (REL 03, CREATED) 01-NOV-1986 (REL 03, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL 35, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCIENCE 132:772-775(1986).

1. TISTE RECTRICTIVE STERMATCHENT AND SOMATIC CELLS.

1. DEVELOPMENTAL STACE HIGHEST EXPRESSION IN LATE PACHYTENE
PERMATCHIES AND POSIMETUTE FORMS PROPE CYSTENES THOUGHT THE INTERMINAL CONTAINS FORMSPAPED CYSTENES THOUGHT THE FUNCLED IN LISTING FOREINS AND PROJECT OF THE PROPERTY FOR PROJECT OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BRAIN,
MEDLINE, 85063850.
HOWELLS P 0, FILPATETOT T 1, PHAIT F MONAHAN
UDENFRIEND S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD: MGI:104628; FENE2.
PROSITE: PS01252; OP10108.
GLEAVAGE ON PAIR OF BASIC
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EMBL; M55181; G201034; -.
EMBL; M19227; G387143; -.
PIR; B35678; B35678.
      POSEN H., DOTO
J BIOL. CHEM.
                                                             SEQUENCE FROM N.A. MEDLINE: 85054888.
                                                                                                                                                   YOSHIKAWA K., FEBS LETT. 24
                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=WISTAR; TIS MEDLINE; 89211398.
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE: 85054887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATTUS NOEVEGICUS (RAT).
BUKARYOTA: METAZOA: CHOPDATA: VERTEBRATA; TETRAPODA: MAMMALIA:
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                                                                                                                                                                                                                                                                                                                                                           YUSHIKAWA K., WI
                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EUTHERIA; RODENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 MYKDS
                                                                                                                                                                                                                                                                                                                         BIOL.
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E. Constitutive C
                                                                                                                                                                                                                                                                                                                         A K., WILLIAMS C., SABOL S.L. CHEM. 259:14301-14308(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
DOUGLASS J., HERBERT E.;
HEM. 259:14309-14313(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
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                                                                                                                                                K., MARUYAMA K., F
246:193-196(1989)
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                                                                                                                                                                            AIZAWA T.,
                                                                                                                                                                                                                                                                                                                                                           SABUL S.L.;
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MET-ENKEPHALIN 3.

MET-ENKEPHALIN 3.

MET-ENKEPHALIN 4.

MET-ENKEPHALIN 4.

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MET-ENKEPHALIN.
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Pred. No. 13;
C. Mismatches
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MISSING (IN REF. 2).
Truefere TEC?2:
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                                                                                                                                                                                  YAMAMOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UPDATE)
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MEHINE, FRIZENT GLE, METER L. HAHLBROCK K., SOMSSICH LE;
ELAN TELL G.GGS 7086/1994).

E SMCT. N. SELTHICALLY BINDS TO THE FUNGAL ELICITOR-RESPONSIVE
THA ELMCMI, "TRANTISTIMA F., FITHE GENE EFE FRIMMIFF
TORRESTIMA FOATION: NUCLEAR.
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                                                                                                                                                      BUKALYOTA OF
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FOR A 1807 A 1807 PARKESSED IN BRAIN, HEART AND TESTIS,

THE N TERMINAL CONTAINS 6 CONSERVED CYSTEINES THOUGHT

TOW OVER IN CLEMETER BANDING AND/OB PROCESSING.

ARTIVE BELLINON FORTHE OPTICAL NUMBER FROM PROPERTY.
                                                                                                                                                                                                                                                                                    modularity 100.0%: Score 27: DB modularity 100.0%: Pred. No. 13: Tenderivative 0: Mismatches
                                             NE BY PATHOMEN INFECTION.

IT - NIAING HAME EAG AND TYS FITH (PHOTEINER) FOMAINS.

THE SEE FROM A FRATEANA REPLAND HATELI, AND MAIZE HOXIA

FOR THE NIAINS FORE A THEOREM ECHANIS.
                                                                                                                                                     TO THE THE (PARSETY) (PETROSELING HORTERSE) APIALES:
                                                                                                                                                                    (PEC 33. (PEALD.)
(PEC 34. LAST SEQUENCE UPLATE)
(EC 34. LAST ANNOTATION UPDATE)
(PEC 31. AST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                          12/11/2
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            SHALLYS AS PROTEINS TRANSCRIPTION REGULATION
                             HIMEOROX, 2:
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MET-ENKEPHALIN 3.

MET-ENKEPHALIN ARG-GLY-LEU.

MET-ENKEPHALIN 4.

LEU-ENKEPHALIN 4.

LEU-ENKEPHALIN 4.

LEU-ENKEPHALIN 4.
A.T HOUR (BY SIMILARITY)
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RESULT 13
YK47_YEAST
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Best Local S
Matches 5
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Best Local S
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REPEAT
SEQUENCE
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DOMAIN
DNA_BIND
DOMAIN
                                                                                                    YKR067W.
SACCHARGMYCES CEREVISIAE (BAKER'S YEASI).
EUKARYOTA: FUNGI: ASCOMYCOITNA: HEMIASCOMYCETES
                                                                                                                                                                                      YK47_YEAST STANDAND: PRT: 743 AA. P36148: 01-JUN-1994 (REL. 29, CREATED) 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE) 01-NOV-1997 (REL. 29, LAST ANNOTATION UPDATE) HYPOTHETICAL 83.6 KD PROTEIN IN CCP1-MET1 INTERGENIO FEGI
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DNA_BIND
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328 MYKDS 332
                                                                                                                                                                                                                                                           750 MYKDS 754
                                                                                                                                                                                                                                                                                     y match
|Local Similarity | 100.0%;
|Local Similarity | 100.0%;
|bos | 5; | Conservative | 0
             1 MYKDS 5
                                                                                                                                                                                                                                                                         1 MYKDS 5
                         Similarity
5; Conserv
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539
743 /
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ilarity 100.0%;
Conservative 0
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A.T HOOK (BY SIMILARITY
A.T HOOK (BY SIMILARITY
CYS-KICH (PHD-FINGER).
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                                                            POTENTIAL.
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                                                                          POTENTIAL.
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2 X 16
4-1.
                                                                                                                                                                                                                                                                                                                                                           3-1.
3-2.
2 x 35 AA
(TYPE C).
3-3.
                                                                                                                                                                                                                                                                                                                                                                                                                  HOMEOBOX.
2 X 13 AA
1-1.
1 2.
2 X 2 AA
2-1.
                                                                                                                                                                                                                                                                                                                                                                                             2-2.
2 x 35 AA
(TYPE C).
                                 Score 1';
Fred. No.
                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                             Score 27: DB
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                           Mismatches
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(BY SIMILARITY).
(BY SIMILARITY).
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38:
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ID P226622
AC P22662
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DI C1-AUG
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XX MEDLINE: 83291825.

XA MEDLINE: 83291825.

XA STATOMI K.I., EVA S., MAEDA M., FUTAI M.;

XI SIONI CHEM. 254:1054-10959(1989).

C :- THIS IS A CATALYTIC SUBUNIT.

C :- SIMILARITY: STRONG TO OTHER ARCHEBACTERIA ALPHA SUBUNITS, ALSO

C RELATED TO THE BETA SUBUNITS OF FO-F1 ATPASES.

RELATED TO THE BETA SUBUNITS OF F0-F1 ATPASES.

REMBL: J04836: G149820: -.

PIR: A34293. A34283.

PROSITE: PS00152: ATPASE_ALPHA_BETA; 1.

PROSITE: PS00152: ATPASE_ALPHA_BETA; 1.

MIP_BIND 229 235

ATP (BY SIMILARITY).

SECURENCE F78 AA: 63678 MW: 41D16AE7 CRC32;
                                                                                                                          Query Match
Best Local S
Matches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDILINE: 98083068.

SADOWSKY M.J. THO 2., DE SCUZA M., WACKETT L.F.,

J. BACTERIOL. 180:152-158(1998).

J. BACTERION. TRANSFORMS N-150PROPYLAMMEDIDE TO GYANURIC ACID AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _PSESD STANDARD: PRT: 403 AA.

052063;
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
N-ISOPHOPYLAMMELINE ISOPHOPYL AMIDOHYDROLASE (EC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATPA_METBA STANDARD: PRT: 578 AA. P22652: 01-AUG-1991 (REL. 19, CREATED) C1-AUG-1991 (REL. 19, LASI SEQUENCE UPDATE) 91-MAY-1992 (REL. 22, LASI ANNOTATION UPDATE) ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34).
                                                                                                                                                                                                                                                                                      HYDROLASE.
                                                                                                                                                                                                                                                                                                                                              ISOPROPYLAMINE.

1 FATHWAY: HEIRE STEP IN AIRAZINE DEGRADATION PATHWAY.

1 SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

1 SIMILERITY: BEYONGS TO THE N-ACYL-D-AMING-ACID DEACYLASE FAMILY EMBI: AF017572: C2736101; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSEUDOMONAS SP. (STRAIN ADP).
PROKARYOTA: GRACILICUIES: SOCIOHACTERIA: AEROBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METHANOSARCINA BARKERI.
ARCHAEBACIFRIA: FURYARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSEUDOMONADACEAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 LYKDS 434
267 LYKDS 271
                                                           1 MYKDS 5
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                                                                                                                             4.
                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                      403 AA: 44938 MW;
                                                                                                                             Conservative
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                                                                                                                                                        88.9%;
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                                                                                                                       Score 24; DB 1; Lc
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 24; DB 1; Lo
Pred. No. 1.6e+02;
1: Mismatches 0;
                                                                                                                                                                                                                                                                                      39909CB1 CPC32;
                                                                                                                                                                                         Length 403;
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Search completed: June

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1999, 10:59:45

Job time: 71 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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## ALIGNMENTS

ORRERO PARKO PARKO	S C O U U U U U U U U U U U U U U U U U U	Ø C	E1 (4)	No. 2 No. 2 No. 2		DR F H A R R			RESU 0755
RHARDITINA BHARDITOTRFA FHARDITITAK, PELLOGERINAR CARDENARDITIS. [1] SEQUENCE FROM N.A. MELLINE, 94150718. MELLINE, 94150718. WILSON F. AITSCHOR F. ANDERSTH F. FAYNES T. BERKS M. BCHEIRID J. WILSON F. AITSCHOR F. ANDERSTH F. COOPER J. COULSON A. GRAXTON M. FORSY T. COOPER J. COULSON A. GRAXTON M. FEAR S. OTT. CONNELL M. SOPER T. COOPER J. COULSON A. GRAXTON M. FEAR S. OTT. CONNELL M. SOPER T. COOPER J. COULSON A. GRAXTON M. FEAR S. OTT. COOPER J. GRAZION E. GRAZION F.	(THEMPLHEL OI, CREATED)  (THEMPLHED OI, LAST SPACENCE UPDATE)  (THEMPLHEL OF, LAST ANNITATION OPDATE)  (MAN SKEBE'S HASIO-HELIX-LOUP-HELIX-LEGGINE SIPPER  (MEAGIOR.  (TIS ELEGANS.  (TIS ELEGANS.)	130 130 132230 FRELIXINARY, FRT; 1758 AA.	1 MYKUS 5	_wery_Match Sect_Limbl_similarityloo_OM, Fred_No. 21: DB 2: Length 198:: Matches 5: Junservative v, Mismatches O: Indels (	SIGNAL. 1 36 POTENTIAL. SIGNAL 1 36 POTENTIAL. CHAIN 37 193 INTERLEUKIN-18. SEQUENCE 193 AA: 22334 MW; 8F226233 GR332;	(1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. YONG D., GUIXIN D., LIHUA H., HAITAO W.: YONG D., GUIXIN D., LIHUA H., HAITAO W.: YONG D., GUIXIN D., LIHUA H., HAITAO W.: SUBMITIED (JUL-1998) 10 EMSL/GENBANK/DDBJ DATA BANKS. EMBL, AF077611; G3348071;	IL18. HOMO SAPIENS (HUMAN). FUKARYOTA, METAGOA, CHOKDATA, VERIERBATA, MAMMALIA, EUTHERIA: PRIMATES: CATAFPHINI: HOMINIDAE: HOMO.	E0.	075599 PRELIMINARY; PRT; 193 AA.

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Hose to Conservative (active)
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Best Lenal Similarity
Mat Les
HAWKING I. HILLIER I. JIER M. JOHNSTON L. JONES M. KEPSHAW T
KIESIEN I. JAISEE W. LAIREILLE P. LIGHTNING T. LOVED C.,
MOMITHAN A. MORITMORE B. O'CALLAGHAN M. PARSON J. PERCY C.,
KIEKEN L. BOSTON A. SAINDERS O' SHOWNKEEN P. SMALDON N. SMITH A
STYNHAMORI TANN F. 1887 P. HIEFPY-MIES I. THOMAS F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMN STANDARD MAILE BRAINS STAALN S
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TWAKEY TA: METAZEAN THORDATA: VENTERPATA: MAMMALTA: EUTHEPTA:
S (VENT.A: STIURGGNATH): MURTDAE: MURTNAE; RAFTUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND SESSION &
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EMBC: 1041020; G1086678;
SEQTENITE (1758 AA; 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ří
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N.V.1998 (TREMBLEEL
-N.V-1998 (TREMBLEEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
21
21
21
21
                                                                                      (TYRIMOLERIL OL OPEATED)
(TYRIMOLERIL OL LAST SEQUENCE OPDATE)
(V FFALCINI FRAME -RE YOUTHOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRECIMINARY
                                                                                                                                                                                                                                                                                                                              TEELIMINARY:
    TYPE AND PART OF THE STRAIN STRAINS AND STRAIN SAFETY S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%: Spark. [100.0%: Pred. No. 2.3e+02; Missorthes 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CANVELVINE LEGIT, ENVERHALL LINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OR, CREATED)
OR, LAST SECUENCE OPPRATE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sec. 22
                                                                                                                                                                                                                                                                                                                              PKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F929D270 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A58A:1164 CRC32:
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                                                                                                                                                                                                                                                                                                                              150 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Longth 1750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
013807
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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BALLETA T P G REMACHA M. SOLEPHMIRA A., JIMENES A.,

GANCIA-GANTALETO T M. POSKOVET T. BEL REY P., REVERTA

RUITBAGO M J., SANS J E ;

SURMITTEL (ULL-1396) T EMEL/DERBARF, TOP TATA FARTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-1998 (TREMBUREL 06 CREATED)
01-JUN-1998 (TREMBUREL 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBUREL 06, LAST ANNOTATION HUDATE)
HYPOTHETICAL 120 7 KD PROTEIN C17H9.10C IN CHROMOSOME
SPAC17H9.10C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOSKOVIC J. SAIZ J.E. SOLER-MIRA A., GARCIA-CANTALEJO
REVUELTA J.L., JIMINEZ A., BALLESTA J.P.G., DEL REY F.,
SURMITTED (FEB-1996) TO EMBL/GENHANK/DDBJ DATA BANKS.
EMBL. 77419 EC17937; -
EMBL: X95644; E223185: -
SEQUENCE 150 AA; 16771 MW; F7086946 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: SOME, TO HUMAN UV-DAMAGED DNA BINDING FACTOR (C1928) ENBL: 298597; B334303; -.
HYDOTHELICAL PROTEIN: DNA REPAIR.
SEQUENCE: 1077 AA: 120654 MW: 89712685 CNCC2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHIZOSACCHAPOMYCES POMBE (FISSION YEAST).
EUKAPYOTA: FUNGI: ASCOMYCOTA: APCHIASCOMYCETES:
SCHIZOSACCHAPOMYCETALES: SCHIZOSACCHAPOMYCETACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKEITON T. CHURCHER C.M., BARREIL B.G., BAJANDREAM M.A., WOOT SUBMITTED (AUG-1997) TO EMBL/GENHANK/DUBJ DATA BANKS.
-1- FUNCTION: MAY HAVE A ROLE IN DNA REPAIR.
                                 01-NOV-1996 (IREMBIREL
01-NOV-1996 (TREMBIREL
51-AUS-1946 (IREMBIREL
                                                                                                                                                                                  Q00026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-972:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                013807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUL-1996) TO EMBLY TO MEANE, DUBJ DATA MANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SACCHAROMYCETACEAE: SACCHAROMYCES
    IMMUNOREACTIVE CLONE GHIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCHIZOSACCHAROMYCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 LYKDS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 LYKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MYKDS 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYKDS 5
                                                                                                                                                                                                                                                                                                                         J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                  PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80.3%;
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06. LAST SEQUENCE UPDATE)
06. LAST ANNOTATION IMPATE)
                            01. CREATED)
01. LAST SEQUENCE UPDATE)
07. LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 1;
Pred. No. 7.4e+(2);
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 24; DB
Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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Lenath 1972:

DB 1; Length 150:

REY F., RUMA IIA

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                  S D R R R R C O O S
                                                                                                                                                                                                                                                                                                                                                                Cuery Match
Best Ichil s
Matches 4
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Best |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL. AF079510, G3511283, EMBL. AF079510, G3511283, EMBL. AF079510, G3511283, EMBL. AF079510, MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-G217B;
CHANDASHERAP P CUPTIS K.C. WEYL G.T. FORAYASHI O
SUBMITTED (MAY-1995) TO EMBL/GENBANK/DJEJ DATA FANKS
EMBL C27598- CAR1430
EMBL C27598- CAR1430
                   SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDINE: 94750718

MILSON P AINSCHICH P ANDERSON K BAYNES C REPKS M BONFIELD J.,

BORTIN TOUNET M CODERY T COOPER J. COULSON A CRAXTON M.,

DEAR S DIT J. DIERBIN P FAVELLO A FULTON L GARDNER A GREEN P.

BAWKINS THILIFE I TIER M TOHNSTON L TONES M., KEPSHAW J.,

KIRSTEN TAISTER N LATTELLES C CALLUNG T DERECT C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HOMO SAPIENS (HUMAN).
EUFABETTA METATIAL THIPFFATA, VERTEBRATA, MAMMALIA, EUFHERTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TREMBLREL, 08, CREATED)
01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDAT
GLIAL CELLS MISSIM PROTEIN HOMOLOG
                                                                                                                                                CAENORHABDITIS ELEGANS
EUKASYTTA METATTA MET
                                                                                                                                                                                   017598;
01-JAN 1998 (TREMBLREL
01-JAN-1998 (TREMBLREL
01-NOV-1998 (TREMBLREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PANENTER Y STEATA S. CHNISHI T. TOOMOTO S. MOSI K
VANASAKI M., EUSHIKI S. ARITA N.
"Molecilat Jlunion if a buman bigin bemelegan of gliat
(bgCMb).".
"The EMFILTINGAKE TOST TATA BANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AJELLOMYCES CAPSULATUS
EUKASYCTA FUNCT, ASCOL
                                                                                                                                    RHABUITINA
                                                                                                                                                                                                                                                01,10,10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIMATES, CATABRHINI, HOMINIDAE HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECHENCE FROM N A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C)
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                                                                                                                                                                                                                                                                                                            LYKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUNTI ASCUMYCETA
NEL AJELLOMYCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    311 AA:
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                  SETACIA MEMATITA SECEFMENTEA, FHABELTIA, PHARDITICA;
RHARDITOIDEA: RHARDITIDAE: PELODERINAE: CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY:
                                                                                                                                                                                                                                            PET IMINAPY
               MORTIMORE B., O'CALLAGHAN M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23305 MW; C9E9A950 CRC32;
                                                                                                                                                                                                                                                                                                                                                                              0 (8)
0 (8)
0 (9)
0 (9)
0 (9)
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. *th 98
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Prod No 1
1: Mismatche
                                                                                                                                                                                     CHEATER)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred No. 3 Re+02,
1: Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  P1181773 TRT32.
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PARSONS J., PERCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPDATE)
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                                                                                                                                                                                                                                                                                                                                                                                        Cenyth 506.
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RESULT
Q18337
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RESULT 10
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Best Local similarity 80.0%;
Matches 1, Conservative
                                                                                                                                                                                             Mutches
                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

MEDLINE: 94150718:

MILY-N & AINSCILLE ANLESELN K. BANNES C. ELEKS M. BONFIELD J.,

MULY-N & CONNELL M. COSEY T. CHORES T. CHUISN A. CENTON M.,

PEAR S. CHIZ. CHEEK E. FAVELLO A., FULTON L. JARLMER A. CREEN E.

HANKINS I. HILLER L. JIER M., JOHNSTON L. JONES M. KERSHAW J.,

KISTEN T., LAISTEE M. LARSELLE F., LICHTNING J., LIOYA

MINURRAY A., MORTIMORE R., C'CALLAGHAN M., PARSONS J. PERCY C.,

KINGHANY A., MORTIMORE R., C'CALLAGHAN M., PARSONS J. PERCY C.,

SONNHAMMER F., SALMINES I., ENWINEER E. LMELLY N. EMITH A.,

SONNHAMMER F., STATEN F. SULSTON J. THIERPY-MIEG J. THOMAS K.,

VAUGIN M. VAUGHAN K. MATERSTON R. WAISON A. WEINSTOCK L.

WILKINSON-SEROAT J., WOHLDWAN F.
                                                                                                                                                                                                                                                                                                                            WATERSTON R.;
STEMITTE (LET 1997) T. FM
EMBL; U42848; G1125818; T.
SECTEMEN (ET AA) 22501
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01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
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NATURE 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; METAZOA; NEMATO PHAROTTINA; PHAROTTINA;
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RHARDITIDAE; PELUDERINAE; CAENURHABDIIIS
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N V-19 (TREMECHEL S. LAST ARROTATION UPDATE)
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ANTHERADA - 189NY (THINESE CAK SILK MOTH).
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NUKASE TA METAS AL ARTHE-959A: TRACHBAIA: HEXAPSUA: INSECIA:
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L MORTIMORE R., O'CALLAGHAN M., PARSONS J., PERCY C.,
LYASAA A., SAUNDERS D., SHEWNKEIN R., SMALTON N., SMITH A.,
E., GALEN K., SULSTON J., THIEKKY MIEG J., THOMAS K.,
VAUNDAN K., WALEKSTON R., WATSON A., WEINSTOCK L.,
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EMRALPELL (L. LAST SEQUENCE UPDATE)

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LEIN HOMELYLL

ELSTERMENT
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01-NOV-1996 (TREMBLEEL 01, CREATED)
01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE)
01-NOV-1996 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
01-NOV-1996 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
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Ol-Jan-1998 (TREMBUREL, 05, CREATED)
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Ol-NAV-1998 (IPEMELPEL, 08, LAST ANNUTATION OPPAIR)
TAILLESS PROTEIN.
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EHKAPYTTA: METARWA: ARTHRWFWWA: TRACHEATA: HENARWWA: TNSE
PTERYSOTA: TIPTERA: HRACHYTEKA: MUSCUMWFFHA: EPHYUNOTDEA:
WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., ELEKS M., BONFIELD J. BURTON J., CONNELL M., COPSEY T., COUPER J., COURSON A., CRAXTON M., DEAR S., DU Z., FUPRIN R., FAVELLO A., FULTON L., GARRINEP A., GREEN P.
                                                                                     SEQUENCE FROM N.A. MEDLINE: 94150718.
                                                                                                                                                                                                                   SEQUENCE FROM N.A MCMURRAY A.;
                                                                                                                                                                                                                                                                                                         RHABDITINA: RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENORHABDITIS
                                                                                                                                                                                                                                                                                                                                  EUKARYOTA: METAZOA: NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC-FINGER. SEQUENCE 450 AA; 50023 MW; 10062F2F 09032:
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PEAM: PEO0105; zf-c4; 1.
RECEPTOR: TRANSCRIPTION REGULATION: DNA-BINDING: NUCLEAR PROTEIN.
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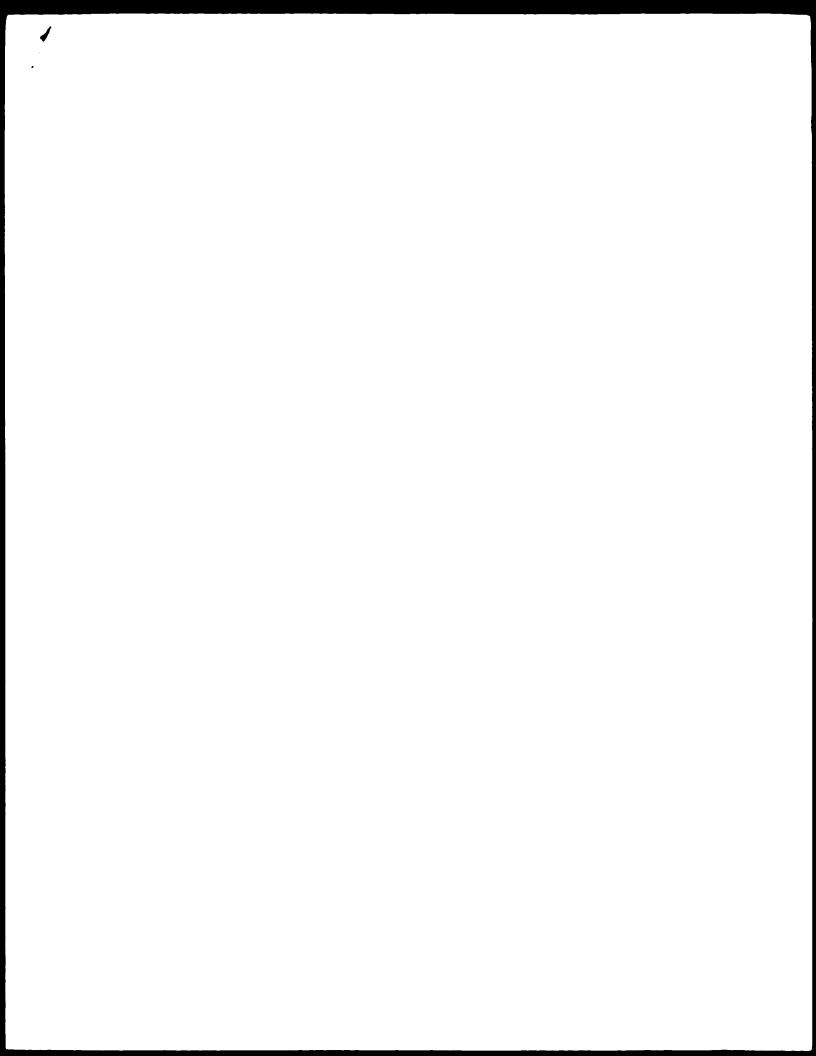
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IB103-1 PROTEIN (FRAGMENT).

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### SUMMARIES

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Kappa	NORUET	1.1	(10) (10) (10)	1.3	40

# ALIGNMENTS

A.Status preliminary translated from GR/EMBL/DDBJ A:Molecule type: DNA A:Moslecule type: DNA A:Residues: 1.37, TE., 199-301; VV., 303-364, 707, 365-489 - GRED A:Cross-references: GB:C01122; NID:q147434; FID:q147435 B:Blattner F F F1:GAM*: TIT: G ROOME, G A. Porca M T. Burland, V.: Biloty, M.: A.; Ross, DJ: Mau, B.: Shao, Y. Science 277, 1452-1462, 1997 A Title The emplate general sequence of Escherithia cult F-12.	5437. NHC 3445 oline permease 15751	C.Path GI-M3: 1789 #shepholocyprovision links: 1383 #text_change 11-Sep-1998 C.Addoesion: A30258, IS4381, E64843 F.Nakaco, T., Yumato, T., Annahu, T. Roll den Genet, 208, 70-75, 1987 A.Title Novleatide sequence of path, the proline carrier gene of Escherichia coli K1 A.Reitheneu manber: A20258; MUID: 87286425	RESULT 2  JGBCPP sedium/proline symportor Escherichia coli w.Alternate names proline carrier protein, proline permeaso, proline transport prote C.Species: Escherichia coli	F F	ing frames are given submitted to EMBL. Levember wrends between two stop codor it can be also submitted to deliberate to deliberate subjects to deliberate subjects to the submitted subjects to the subjects of the subject of the subjects of the subjects of the subject of	A:Title: Analysis of the protein coding content of the sequence of human critame alowi A:Reference number: \$09749; MUID:90269039 A:Accession: \$09808 A:Status: Authority and services and shown translation not shown A:Molecule type: DNA	5 protein  The 21 Aug 1998  Cormy, B. Horst 1	reductions (FO 1.17 A.17 Living Abrilla - Bompo (mirromovas) vide
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NASA Certain e naces: hypothetical protein JCG27
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Li Cos L. Jan Li OS #Lepaence revision l'Odan 1965 #text_change 04 Sep
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R:Arriza, J.L.; Weinberger, C.; Cerelli, G.; Glaser, L.M.; Hundelin, B.L.; Hensman, D. Science 227, 268-275, 1987
A.Tille, Cloning of human addered besetticoid receptor complectors; IAVA, structural an A. Reference comber, A29513, M910.87263386
A:Accession: A29513
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A:Residues: 1-33 cPAR:
A:Residues: This peptide has antimicrobial activity.
C:Comment This peptide has antimicrobial activity.
C:Superfamily: ranalexin precursor; dermorphin precursor amino terminal lawelos;
C:Keywords: disulfide bond: skin
F:27-33/Redion: rana box motif
                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 31-Mar 1990 #sequence_revision 31-Mar-1990 #foxt_chande 13-Sep-1998
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N:Alternate names: aldosterone receptor
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A;Accession: PC2302
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R:Park, J.M.; Jung, J.E.; Lee, B.J.
Biochem. Biophys. Res. Commun. 205, 948-954, 1994
A;Title: Antimicrobial pertides from the skin of a Korean From,
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C.Keywords: disulfide bund: skin
F.27-37/Region: rana box motif
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R;Park, J.M.; Jung,
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C;Date: 25-Feb-1995 #soquence_remision 25 May-1995 #toxt change
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A:Pesidnes: 1:37 *FAE*
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| 25-ლიზ-1995 #დიქსითბი_rovision 26-May-1995 #'oxt_obundo (რიტpr-)სოწ
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Biophys Res Commun 205, 948-954, 1994
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0; Mismatches
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RESHIT R
S10220
sodium(thiller symperto) - Salmenella typhimurium
sodium(thiller symperto) - Salmenella typhimurium
N.Alterate agree proline agreer protein, proline permease, proline transport protein
CiSpecies, Salmonella typhimurium
CiSpecies, Salmonella typhimurium
CiSpate: 12-pob-1002 **seguence_remision 12-pob-1993 **text_change 13-Sap-1908
CiAccessian, S10220; N39192, S03816
CiAccessian, S10220; N39192, S03816
CiAccessian, S10200; N39192, S03816
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AsiGener was TVE-117184 MIM 20150
AsiGener was TVE-117184 MIM 20150
AsiGener was transforming protein homology
CoSuperfamily: Unassigned eith related proteins; erbA transforming protein homology
CoSuperida DAN binding, transcription regulation; zinc finger
Es601-8800000016 ErbA transforming protein bimology EPBA>
Es603-627580916 Libb finger
Es603-627580916 Libb finger
Nucleic Acids Res. 18, 3057, 1990
A:Title: DNA sequence of the puth gene from Salmonella typhimurium and
A:Reference cumber, 318229, MUID:98272423
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C:Superfamily: G
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A:Molecule type: DNA
A:Residues: 1-2718 <PRA>
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A:Title: Nucleotide sequence of the Paramecium A:Poferono number: 8,7475 Mrip 8706034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G surface protein - Paramecium primaurella (SGC5)
C:Species: Paramecium primaurella
C:Dato: al-Mar-1999 #soquopoc_pocisino al Mar-1999
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A:Residues: 1-984 MARES
A:Cross-reforences: 08-M16801: NID a187460.
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File 147. Domain transmembrane *status predicted <TMC4*
Fil63-185/Domain transmembrane *status predicted <TMC4*
Fil63-191-210/Domain transmembrane *status predicted <TMC5*
Fil23-255/Domain transmembrane *status predicted <TMC5*
Fil27-297/Domain transmembrane *status predicted <TMC7*
Fil17-353/Domain transmembrane *status predicted <TMC8*
Fil27-395/Domain transmembrane *status predicted <TMC9*
Fil27-395/Domain transmembrane *status predicted <TMC9*
Fil27-395/Domain transmembrane *status predicted <TMC9*
Fil28-444/Domain transmembrane *status predicted <TMC1*
A.Description outalyzes the problem for Nat Department Michael Interchaism C.Superfamily proline carrier protein
C.Superfamily proline transport sodium transport system, transmembrane protein
P.2-26/Domain: transmembrane #status predicted <TM2>
F.40-73/Domain: transmembrane #status predicted <TM2>
F.40-73/Domain: transmembrane #status predicted <TM3>
F.120-147/Domain: transmembrane #status predicted <TM3>
F.120-187/Domain: transmembrane #status predicted <TM5>
F.21-210/Domain: transmembrane #status predicted <TM5>
F.21-210/Domain: transmembrane #status predicted <TM6>
F.21-210/Domain: transmembrane #status predicted <TM8>
F.21-210/Domain: transmembrane #status predicted <TM8>
F.21-210/Domain: transmembrane #status predicted <TM8>
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N/Alternate names: proline permease
C/Species - Pseudomonas fluorescens
G:Date - 20:Feb 1905 #sequentry Fred Sign 20:Feb 1907
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RiHahm, D. P.; Myors, P.S.; Mont. C.P.; Maloy,
Mol. Gen. Genet. 213, 125-133, 1988
A.Title: Regulation of proline utilization in
A.Reference number. Stowle, MUII:29127131
A.Recession: SO3816
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A;Mulecule type: DNA
A;Residues: 1-494 -HOS
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A;Accession: JC2382
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Similarity 100.0%; Prod. No. 1.5e+02;
5; Conservative 0, Mismatches 0,
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The constant Dec List asseptioner revision 04-bon-1442 #fext_change 13-Sep-1448

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Talled [19 Feb = 60] #leephonco_nertwire 19 Mark 1997 #text_phange 13-Sep-1999
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Rizhou, Q.Y.: Li, G.; Glah, M.E.; Johnson, R.A.; Stiles, G.L.: Givelli, T. Proc. Natl. Acad. Sci. U.S.A. 89, 7432-7436, 1992
A;Title: Molecular cluming and characterization of an adenosine receptor: the A4 aden A:Beference number: A46152, MUID:93366475
A;Accession: A46152
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F:45,42,161.21/Finding site: carbohydrate (Asu) (considered Fidered Status predicted <TMC)
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FERS Lett 284, 155-156, 1991
A.Title. Molecular closing of a sound potation 3-proto-in social discognic captorised d.
A.Peforence number: SIT177; MSID:01295122
A.Accession: S17177
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A, Closs-references: 35 MM41F2: NID-g200724, ETC-g481212
A) Experimental source: brain
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Sep-1993 #sequenco_rovision 19-Nov-1994 #:oxt_chungc 13-Sep-1998
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P.Eleischmann, E.D. Adams, M.D. White, G. Clayton, E.A. Kitkonsk, E.E. Kollavade G.Godyne, J.D. Scott, J. Shirley, E., Liu, L.I., Glodek, A., Kelley, J.M., Weldman Science 259, 496-512, D. 195 Actuations Cotton, M.D. Utterback T.P. Hanna, M.C. Nguyen, D.T.; Saudek, D.M.; Rr. V.: Fraser, C.K.; Smith, H.O.; Venter, J.C. Affilte: Whole genome random sequencing and assembly of Haemophilius influenzae Rd.

hypothetical protein WIC342 Haemophilus influencae (strift Pd PW20) C;Species: Haemophilus influencae C;Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 30-Jun-1998 C;Accession: H64148

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submitted to GenBank, May 1998
A: Description. Genome sequence of an obligate intracellular pathogen of humans: Chlamydi A:Accession: E71484
A:Status: preliminary A:Molecule type: DNA A:Residues: 1-245 CARNA A:Cross-reference: CP:AECO1228. GB:AECO1273, NID:33229126, PID:g3329130
A:Experimental source: Serotype D, Strain UW-3/Cx
C:Genetics:
A:Gene: pyrH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable UMP kinase - Chiamydia trachomatis (serotype D, strain UW3/Cx) C:Species: Chiamydia trachomatis C:Date: 13-Sep-1998 *sequence_revision 13-Sep-1998 *text_change 13-Sep-1998 C:Accession: E71484

P:Stephens P.S. Kalman, S.; Lammel, C.J.; Fan, J.: Marathe, R.; Arawind, 1
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Title: Perfect score: US-09-030-061-5 26 1 STLSC 5

Scoring table: BLOSUM62

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Database : A\_Geneseq\_34:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is forted by analysis of the total score distribution.

## SUMMARIES

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PT and novel hormone receptors  PS Claim 17: Fig IV-2(B)-1 and -2: 243pp; English.  CC PNAs encoding hormone receptors and the burmone receptors licenselves are CC claimed. The ENA cun be used to make the hormone receptor proteins and CC functional modified forms in quantities not previously possible. The CC receptor proteins can be used to screen epds, for receptor-catonist or tweettor-anonymist intiff; They can also be used to 323ys Sequence 984 AA:	(SALK) Halk inst for Biol Stud.  Evans FM. Weinberger CA. Hollenberg SM. Giguete WPI, 88-133242/19.  N-PSEB: N40920.  FOURNITHE TAX AND ALLEBORY FEEDBALE TO SEE COMPTISING GIVEN CANADA COMPTISING GIVEN COMPTISING GIVEN CANADA COMPTISION	0927  P80927;  P80927;  29-DEC-1990 (first entry)  Segioner of the human minerallicational receptor Human minerallicational receptor Human minerallicational receptor Human sapiens.  W08803168-A.  05-MAY-1988  23-021-1987; US-108471.	44 24 97 3 1106 1 E93690 45 23 98.5 107 1 W00049 ALIGNMENTS
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E25202 standard, Frotein; 509 AA. R25202; 04-JAN-1993 (first entry) Human PH-20 protein H18. Sterm surface Frotein, contraceptive, vaccine.

W09210569-A. 25-JUN-1992. 04-DEC-1991, 14-DEC-1990. Homo sapiens.

US-627782

(HYGO-) HMIV CONNECTICUT. Myles DG, Primakoff P; WPT: 92-234625/28.

OR N-FSEE: 025302.

PT Sperm cell surface protein FH-2C and DNA encoding it for use in FT a centraceptive vaccine
FT a centraceptive vaccine
FS Example, Fig 4. 38pp; English.

Other sequence is that of number sperm surface protein PH-2C type H18 of the sequence is that of number vaccine. The vaccine is longer for lasting that the end contraceptive with surgical sterillsation. The new for contraception such as occurs with surgical sterillsation. The new flexibiting that the end is more effective than other methods of contraception and is more convenient. The sequence of H10 between the protein is identical to that of the partial sequence, H20 between the condex amino acids 497-511, and H16 encodes amino acids 497-511, and the condex amino acids 497-511.

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Mir March 5 Tomographics
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P252 (S
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2-2 Prij/10
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[artity [100.0%; Pred, No. 2.5e+02;
[amtition 0] Mismitthen 0.
                                                                                                                                                                                                                                                    (treat entry)
As not been some HTB).
The process to till sation: sperm surface protein:
The process to the HTB.
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     with the test reducing sperm-equitision
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Best Local Similarity
Matches 5: Conserv
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Best Local Similarity 100

Matches 5. Conservative
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Example 4; Fig 5; 79pp; English.

Sperm surface proteins or peptides stimulate an immune response to produce antibodies which block sperm-egg fusion and provide contraception. Pref. sperm surface proteins are the 185-2 and 185-
                         02-MAR-1995.
19-AUG-1994; U09395.
20-AUG-1993; US-110158.
(OKLA ) UNIV OKLAHOMA STATE
MCCYCT_RP, Pan J:
                                                                                                                                                                                                   megakaryocytes; rheumatoid atherosolerosis; banterial
                                                                                                                                                                                                                                                                                        R65216;
04-0CT-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contraception. Pref. s
sperm surface proteins.
Sequence 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1993.
10-UUN-1993; U05640.
12-UUN-1992; US-897883.
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                                                                                                                                                     WO9506118-A.
                                                                                                                                                                                                                                                                              P-selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contraceptive vaccine for reducing sperm-egg fusion peptide from sperm surface protein which stimulates
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WPI: 94-007200701.
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W09325233-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human PH 20 (derived from partial clone H16). FH:30, contraceptive, fertilisation; specm surface protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R47349 standard; Protein; 275 R47349;
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                                                                                                                                                                                                                                                  Control clements,
                                                                                                                                                                                                                                                                                                                                              R65216 standard; Protein, 830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-FSDB; Q54635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccine; sperm-eqq fusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 STLSC
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     95-106847/14
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                                                                                                                                                                                              gene expression, endothelial colis;
heumatoid arthritis; ischaemic injury,
bantarial sapsis; tumbur metastuses.
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Best Local
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Best Timpl Strillaning 100
Matches C. Conservative
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Claim 1) Figure 1) 39pp; English.

A3 adenosion receptors produced from cloned genes may be used to softer o compounds for A3 adenosion receptors activity, or for determining the amount of adenosine against or antagonist drug solution. The DNA or its fragments may also be used as probes determine tissue distribution of the receptors, to detect the first-order or absence of the gene or in RFLF to detect genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expression notice alements in the 5% flanking region of the first of the first property of the expression in endsthellal cells and mena-karponyte(s). English. The sequence is that of the Posabe to gardened from endothellal cells, determined from a composite of four overlapping cDNAs. lambda SREEL Lambdu SREEL the sequents gave or its fragments may be used to inhibit recitatin expression, thus controlling inflammatory and haemostatic processes in e.g. Theumatoid arthritis, ischaemic injury. Sequence 83% AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clvell
02-SEP-1996 (first edtry)
Interferor damma prodoction inducer protein
Interferor damma prodoction inducer protein
Interferor damma, inducer, IFNgamma; immunocompetent cell; antiviral;
antitumgur, ant Septic, immunocredulatory; platejet increasing agent
therapy; provention, outditons administum, renal cancer; brain dancer
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03-MAR-1992: US-847563.
02-AUG-1993: US-101435.
UTV-F.; TMIN TETTIN HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1996 (flist wotiy)
Rat A3 adenosine receptor:
                                                                                                                                                  R92506 stundard. Protein; 157 AA R92506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                             154 SILSC 168
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Fred. No. 7.2
0; Mismatches
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Fred W. 24+52;
Mismatches 0: Indels
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        (HAYR ) HAYASHIRARA SEIRUTSU KAGAKU
I Eukuda S. Kubuo K. Kumikata I. Kuli
Taniguoti M. Tanimata T. Tarigao K. (
WPI: 96-052837/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marches
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                                                                                           10-NOV-1995; 308055.

15-NOV-1994; JP-304203.

23-FEB-1995; JP-058240.

10-MAR-1995; JP-078357.

18-SEP-1995; JP-272952.

23-SET 1995; JF-274988.
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Chaim 2: Page 2: 30pp Emplish.

This sequence represents the interferen gamma (IFNgamme) inducer protein of the invention. This protein induces IFNgamma production in impurpecempetent cells. The protein is useful as an antiviral, intitudus, unlikefile inmunicagulatory and platelytic invasing grot. It can be used for theating of preventing AIDS, ended to any engine number read or theating of preventing AIDS, ended to represent and allergy. The protein data also be used to induce IFNgamma production in whitness tells. The iFNgamma inducer strongly induced introduction in the first can also be used to induce IFNgamma production in whitness tells. The iFNgamma inducer strongly induced introduction in the first calls and the inducer strongly introduced in adaptive immunotherapy in tumours. The DNA encoding this sequence can be used to produce the protein which can then be purified by assayed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein that induces gamma interferon product in immonocompetent cells - used e.g. as antiviral or antitumour agent, also induces cytotoxicity of killer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tanimute T, Torigoe
WPI; 96-070177/08.
N-PSDB; T92506.
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Filler ( v.l), lotoxivali, 1, 12-1, tambut bocksis () (1), 187;
adoptivo įmmunothorapy, monocional antibody.
                                                                                                                                                                                                                                                                                                         29-SEP-1996 (first entry)
Mouse mature interferon-gamma inducer protein.
Interferon-gamma inducer protein: IEN-gamma: antiviral viruoide:
antitumour: antibactorial: immunoregulator: adoptive immunothorapy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HAYB) HAYASHIBARA SEIBUTSU KAGAKU. Kohno K, Kunikata T, Kurimoto M,
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14-JUL-1994: JP-184162.
10-FEB-1995: JP-045057.
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                                                                                                                                                                                          EP-712931-A2.
22-MAY-1996.
                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                          therapy; cancer.
Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                         R99559 standard; Protein: 157
                                                                                                                                                                                                                                                                                                                                                                           , 6<u>5</u>5663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     using monoclonal antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 STLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local similarity
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interferor gamma productinducing polypoptide
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1.65.02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of the Lippe Alphanese. The sequence interteron-gamma is defined to the companion which induces interteron-gamma is define the companion to the protein may be used as the sequence of the drug for the prevention and treatment of the sequence of the companion of the sequence of the sequence
No. 1910
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A condition of private (Pintsty) induces interferon-gamma (IFN-gamma) in an interferon management relia. Its sequence was deduced from that the NA condition (24A) isolated from a mouse library. Secretina: 15FM inuma inducer protein can be produced in high yields conditions: 15FM inuma inducer protein can be produced with a vector various of the color. Essentichia collictransformed with a vector carriering the color.
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A 180 Hollowing to the which induces interferon-gamma
and information is selected that the unduces interferon-gamma
and information of the manifestant functions, viral, bacterial or
any first discusses
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tune to competent oil; malignant tunour
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30955, df
378.37
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                          unduction factor 2 (1218-2) 81401 curtiant.
Induction factor 2: 1918-2: leucocyte: lymphocyte:
Liberation, 4111erentiation, materation, tissue d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          [00.0%] Score 25; DB 1; [00.0%] Pred. No. 1.56*02;
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Pred. No. 1.6
9, Mismatches
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ches 0:
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Query Match
Best Local Similarity
Thehes 5; Conserv
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Claim 1: Page 46: 60pp; English.

Claim 1: Rage 46: 60pp; English.

This is the protein sequence of interferon gamma industing testor?

(IGIF-2). An IGIF-2 variout (W3175) and an IGIF variout (W22449),

which may be an alternate transcript, also exist, Probes derived from
the nuclei, acid sequences can be used to public, the expression of
IGIF-2 in conditions that are associated with inflammation or aberram
expression of IGIF-2. The protein can be used to screen for compounds
that interact with IGIF-2, such as antibodies, antanopists or other

This components of the protein can be used to screen for other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This protein sequence represents an interieron wamma inducing factor... (ICIF 2) variant, identified from a liver cDNA library. This acquence differs form ICIF-2 identified from a Tlymphocyte cDNA library (W2244) in that amino acid idd is found to be changed from Arq to lie. A second variant, W2242, lie. Asks. Proceed delived from Arq to lie. A second sequences can be used to quantify the expression of ICIF-2 in conditions that are associated with inflammation or abeyrant expression of ICIF-2. The protein can be used to screen for compounds that introduced with ICIF-2, such as antibedies, antagonials or other liels to see this protein can also be used to diagnose, prevent or treat ICIF-2 induction of protein can also be used to diagnose, prevent or treat ICIF-2 induction of protein can also be used to diagnose, prevent or treat ICIF-2 induction of proteins and account the contraction of the contraction of the contraction of the contraction of proteins as activities to the contraction of proteins.
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                                                                                                                                                                                                                                                          with inflammation
Claim 1: Page 46;
This is the protei
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N-PSDB; T74987.
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20-DEC-1996; U20432.
29-DEC-1995; US-580667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interferon gamma inducing factor-2 (IGIF-2) protein.
Interferon gamma inducing factor-2, TGIF 2, leading to limphoryte;
inflammation; proliferation; differentiation; maturation; tissue damage.
                                                                                                                                                                                                                                                                                                                                                              Novel Interferon gamma inducing factor 2—used to screen for rompeyings to diagrass, treat or present tissue dumage associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INCY-) INCYTE PHARM INC
Cocks BG, Coleman B, H
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W09724441-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: This sequence does not appear in the specification; it has been made by mudifying the ISTE'S sequence presented in WSSS47. Sequence 193 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nevel interferon gamma inducing factor-2 - used to screen for compounds to diagnose, treat or prevent tissue damate users in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; 174988
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20 DEC 1996; U20432.
29-DEC-1995; US-580667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3: Page -: 60pp: English
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100.0%;
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Pred. No. 1.9e+02;
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W27056
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Best Local
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26-SEP 1996. 306697.
20-SEP 1996. 306697.
28-SEP 1995. UP-270725.
29-FEB 1996. UP-270725.
29-FEB 1996. UP-270725.
ANITA F 1996. UP-367434.
F1678. F 1996. UP-367434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human protein that induces interferon-gamma prodo in inmunocompetent cells - useful for adoptive immuno:therapy of tumours and as antimicrobial agent etc.

Disclosure, Fage 22: 26pp; English.

The present sequence represents a novel protein from mouse liver cells, which induces interferon-gamma (IN gamma) production in immunocompetent cells. This protein enhances cytotoxicity of killer cells and induces their formation. It is used as an antioncotic agent for antitumour immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and including anti-AIDS) or antibacterial agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression or activity. The protein can also be used to diagnose, prevent or treat IGIF-2 induction of proliferation, differentiation or maturation of Leuroptes of Emphasytes, especially in relation to dissue dumage associated with inflammation.

Sequence 193 AA:
                                                                                                                                                                                                                                                                   and in the treatment of atopic or immune system diseases, e.g. asthma, hayfever or rheumatism. When formulated with interleukin-3, it is also sed to treat leab gravina and threadwayt.gravina associated with radiotherapy or characterially introduced and other cancers. When used in antitumour immunotherapy of bucksomia and other cancers. When used the immunotherapy this novel protein significantly improves the immunotherapy to interleukin-2 (II-2), compared with use of II-2 alone, either when administered to the patient (before administration of II-2) is the figure to the patient (before administration of II-2) is the figure to the patient (before intended for return to the patient) are being grown sequence. 157 AA:
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WPI: 97 205381,/19.
N-PSDB: T60536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 JAN 1998 (first entry)
Wouse interferon-gamma inducer protein.
Interferon-gamma, IFN gamma; antiviral; antioncotic; radiotherapy; immunoregulatory; antitumour agent; chemotherapy; leukopaenia; thrumbubytepaenia, immunocompetent cell, asthma, hayfever, rheumatism, interleukin, killer cell
W27056 standard, peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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Clarity 100.0%;
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Pred No 1 K
O, Mismatches
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Pred No 1 4e+02;
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PR MANDE PA (1863)/4]

EN MPI, 97-(4863)/4]

FI Kricks F, Stadler B.

PI Movel in American Springlish.

Co min peptide sequence (Without the terminal cystelor residues) was continuously by sequence (Without the terminal cystelor residues) was synthesised of displayed by RSWI7 minectope phages. The peptide was synthesised of with the additional cystelor residues for circularisation. The peptide was used in a new immunogenic molecule for vaccination against one molecy of a peptide minicking the natural epitope on human peptide inmunoglobulin E (19E) recognised by the monoclomal anti-human IE anti-human in E anthody SSWI7 and a molecy capable of eliciting an immune response of anthody SSWI7 and a molecy capable of eliciting an immune response of against the peptide. The peptide is used in the preparation of vaccines or used as vaccines for the generation of anthodies which inhibit most of the used as vaccines for the generation of anthodies which inhibit most of the "classical vaccine" approach, as no light performs the property of approach, as no light protein fragments are property to an approach as confidence in the compared to the property to an approach as confidence in the compared to the property to these minectopes is suffered to include the property to the sequence of the compared to a property to the sequence of the compared to a property to the sequence of the compared to a property to the sequence of the compared to the property to the sequence of the compared to the property to the sequence of the compared to the property to the sequence of the compared to the property to the sequence of the compared to the property to the sequence of the compared to the property to the sequence of the compared to the compared to the property to the sequence of the compared to the comp
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01-APR-1998 (first entry)
101-APR-1998 (first entry)
Peptide Asgardan #4 displayed by PSW17 mimactope phages.
Peptide immunogen, vancination, allergy, epitope, IgE, immune response:
immunoglobulic E, and k-dy PSW17, atuple dermatilis, PSW17 winestope;
antibody: mast cell; bascphill immunisation, mimochype phage; circular.
kegior
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### SUMMARIES

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  TO EMBLIGHTENHANE/TERRITORIA PANES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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STANJARINASTRU
TVI INSTRU
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D. Mismatches
                                                                                                                                                                                                                                                                                                                                        FRT:
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Q93238
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Best Local Similarity
5: Consor
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Best Local
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DOMAIN 319 432
TOMAIN 334 441
LOMAIN 565 566
SECCIENCE 747 AA. 93795 9
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINE: 94150718

WILSON F. AINSCOUGH F. ANDERSON K. RAYNES C. PERKS M., BONFIELL I.

BUXION J. CONNELL M. CODSEY I., COOPER J., COULSON A., CHAXTON M.,

BUXION J. CONNELL M. CODSEY I., COOPER J., COULSON A., CHAXTON M.,

ECAR S. TH. SUFFEN F. LATELLE P. LIGHTNING J. LOVE M., KERSHAW J.,

HAWKINS T., HILLIER L. JIER M., JOHNSTON M., FORES M., KERSHAW J.,

KIPSTEN I. (AISTER N. LATREILLE P. LIGHTNING J. LOVE C.)

MCMUPPAY A. MORTIMORF B., CYCALLAGHAN M., PARSONS J., PERCY C.,

MCMUPPAY A. MORTIMORF B., CYCALLAGHAN M., PARSONS J., PERCY C.,

SONNHAMMER F., STADEN P., SULCTON R., WATERBY M. TEC.

VAUDIN M., VAUGHAN K., WATERSTON R., WATSON A., WEINSTOCK L.,

WILKINSON-SEPOAT J., WOHLDMAN P.,

WILKINSON-SEPOAT J., WOHLDMAN P.,
      016644 FRELIMINARY) PRT; 332 AA.
016444;
01-JAN-1998 (IFEMELREL 05, CREATED)
01-JAN-1998 (TREMBLREL 05, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANN:TAITON UPDATE)
E56012.3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             093238 FRELIMINARY, FRT. 925 AA.
093238: O1-FEB-1997 (TREMBLREL. 02, CREATED)
01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDAIE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOIALION UPDAIE)
                                                                                                                                                                                                                                                                                                                                                     "2 2 Mb of contiguous audientide sequence from chromosome III of elegans.";
elegans.";
NATURE 368-32-38(1994).
EMBL: Z78415: E259012: -.
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                                                                                                                                                                                                                                                                                                                                        SECTENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. WHITE S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHARDITINA: RHABDITOIDEA; RHABDITIDAE; PELODERINAE; CAENCRHABDITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EUKARYOTA: METAZOA: NEMATODA: SECERNENTEA: RHARDITIA; RHABDITIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAENORHABDITIS ELEGANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              555 STLSC 559
                                                                                                                                                                                        872 STLSC 876
                                                                                                                                                                                                                       1 STLSC 5
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5; Conservative
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                                                                                                                                                                                                                                                         Conservative
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E259012: -.
A: 98240 MW:
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ETT41947
                                                                                                                                                                                                                                                      Score 26; DB
Pred. No. 3.1
0; Mismatches
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CAENOPHABITTIS ELEGANS

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DET PRACES RAPERAL RAPERA RA
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Best Toral :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BRISTOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     018276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBMITTED (JUL-1997) TO EMBL/GENBANK/DDBJ DATA BANKS EMBE, AFOLUGIJ, JD315672, SEQUENTE 332 AA. 37377 MW. F256779D CPC32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WATERSION R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAULEY A., MAGGI I. HARPER M.:
SUBMITTED (AUG-1947) TO EMBLAGENHANK/BOBJ DATA BANKS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVince See 35 sevideds
                                                                                                                                                                                                                                                                                                                                         WILSON R. JAINSCOUGH R., ANDERSON K., BAYNES G., BERKS M., BONFIELD J., BERTON T. CONHELL M., COPSEY T., COOFER T., COULSON A., CRANTON M., BURTON T., CONHELL M., COPSEY T., COOFER T., COULSON A., CRANTON M., BURTON T., CONHELL M., FULTON L., GARDNER A., GREEN P., LEARNESTON T., LICHTON L., JONES M., KERSHAW J., HANSTER N., LATEFILLE P., LIGHTNING J., LLOYD C., KINSTEN N., TARTSER N., LATEFILLE P., LIGHTNING J., LLOYD C., MCHURRAY A., MORILMAKE E., COLLAMBIAN M., TARSONS T., PEPCY CO., MCMURRAY A., SAUNDERS D., SHOWIKEEN R., SMALDON N., SMITH A., SCHWIKEEN E., STALEN S., SHOWIKEEN R., SMALDON N., SMITH A., SCHWIKEEN E., STALEN S., WAIERSTON P., WATSON A., WEINSTOCK L., VAUGIN M., VAUGHAN E., WAIERSTON P., WATSON A., WEINSTOCK L., WAIERSTON P., WATSON A., WEINSTOCK L., WAIENSTON P., WAIENSTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TREMBLREL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N A MEDIINE: 94150718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EUKARNOTA, METAZOA: NEMATODA: SECEPNENTEA: RHABDITIA; RHABDITIDA;
RHABDITINA, PHABDITOTDEA: PHABDITIDAE: PEUODERINAE: CAENORHAADITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAENORHABDITIS ELEGANS
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                                           NATÜRE 368.32 38(1994).
-:- SUBCELLICAR FORALION. INTESPAL MEMBEANE PROTEIN (RY SIMILARITY).
-:- SIMILARITY. EFFICAGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
EMBL. 293307: E1186516: -.
          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tes 5; Conservative
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RHABDITOIDEA, KHAEDITIDAE: PELICEPINAE: CAENORHABDITIS
     FS00236; NEUROTR_TON_CHANNEL;
                                                                                                                                                                                                                                                                                                   contiguous nucleotide sequence from chromosome III of \dot{c}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 05, CREATED)
. 05, LAST SEQUENCE OR, LAST ANNO
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LAST ANNOTATION UPDATE)
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DU KARARARA ROCCO OG DU DAC
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Q47551;
Q47551;
Q47551;
Q47551;
Q1-NOV-1996 (TREMBLREL. (
Q1-NOV-1998 (TREMBLREL. (
C1-NOV-1998 (TREMBLREL. (
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POSISYNALIIC MEMBKANE, ICHIT CHANNEL: GLYCTPKCIEIN, IKANEMEMBBANE,
SEQUENCE 545 AA, CIECI MW, 25207F18 CKT30:
                                                                                                                                                                                                                                                                                                                                                                                                                                        047552;
047552;
01-NOV 1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Evolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of Salmonella and Escherichia coli.";
J. BACTERIOL. 174:6886-6895(1992).
EMBL: L01133; G147437; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FECLINE PERMEASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 489
SEQUENCE 489 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESCHERICHIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTER!A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE: PS00456; NA_SOLUT_SYMP_1; PROSITE; PS00457; NA_SOLUT_SYMP_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 93015751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00474; SSF;
                 "Evolutionary genetics of the proline permease gene (putF) and the control region of the proline utilization operon in populations of salmorella and Eacherichia coli."

J. BAJIERIJ. 124.4886 (1902).

EMBL. 101102. 6147443.
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                                                                                                                                                                                                                                                                                                                                                                                        PROLINE PERMEASE (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NCV-1998
EMBL, L01102; G14/444; -. progritt: P800456; NA_SOLUT_SYMP_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 SILSC 344
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                                                                                                                                                                                    SEQUENCE PROM N A.
MEDLINE: 93015751
                                                                                                                                                             NETSON Y , SELANDER P K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 26; DB 9; ilarity 100.0%; Prod No. 1.8e+02; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           (TREMBIREL)
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01. LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDATES
                                                                                                                                                                                                                                                                                                                                                                                                                   01, LAST SEQUENCE UPDATE)
08, LAST ANNOTATION UPDAT
                                                                                                                                                                                                                                                                                                              CAMMA SUBDIVISION: ENTEROBACIERIACEAE.
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Pred. No. 1.9e+02;
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OF NOV-19 OF (TREMBLREE, OF, LAST SECUENCE UPDATE)
OF THE VEHICLE OF THE SECUENCE OF THE
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i three terrotion of the proline utilization operon in populations of
the arotherichia coli,";
EFC-55. 174:5886-6895(1992).
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RESULT 13
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Best Local :
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"Evolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of Salmonella and Escherichia coli.";
                                                                                                                                             Q54979 PRELIMINARY; PRT; 489 AA.
U54979;
01-NOV-1996 (TREMBLREL 01, CREATED)
01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPDATE)
                                       SEQUENCE FROM N.A.
MEDLINE: 93015751
NELSON K., SELANDER R.K.;
                                                                                               BACTERIA: PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROKACTERIACEAE:
                                                                                                                                   PUTP
                                                                                            SALMONELLA
                                                                                                                     SALMONELLA SP
                                                                                                                                           PROLINE PERMEASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                    WFLSON K., SELANDER R.K.;

"Frolltionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of salmonella and Escherichia coli.";

1. BACTEPTOL 174-FRRC.£895(1992).

EMBL; L01135; G154292; -
EMBL; L01135; G154292; -
EMBL; BRO0456; NA_SOLUT_SYMP_1; 1.

PROSITE; PS00457; NA_SOLUT_SYMP_2; 1.

PFAM; PF00474; SSF; 1.
                                                                                                                                                                                                                                                                                                                                                                                  SECHENCE
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Q54978;
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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SEQUENCE 489 AA;
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489 AA; 52857 MW,
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100.0%;
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Pred. No. 1.8e+02;
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Pred. No. 1.8e+02;
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RESULT 15
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EMBL: 101137; 6154294.

PROSSIB: PS00450; NA_SOLUT_SIMP_1,

PROSSIE: PS00457; NA_SOLUT_SIME_1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NEISON K. SELANDER R K.;

"Evolutionary genetics of the proline permease gene (putP) and the control region of the proline utilization operon in populations of Salmonella and Escherichia coli.";

"BACTERIOL 174:6886-6895(1992).

EMBL: L01139: G144296;

PROSITE: PS00455: NA_SOLUT_SYMP_1: 1.

PROSITE: PS00457: NA_SOLUT_SYMP_2: 1

PEAM: PF00474: SSF; 1

PEAM: PF00474: SSF; 1

PEAM: PF00474: SSF; 1
                                                                                                                                                                                                                                                054981 PRELIMINAPY: PPT: 480 AA 054981; 01-NOV-1996 (TREMBLEEL 01, CARATED) 01-NOV-1996 (TREMBLEEL 01, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLEEL 08, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O1-NOV-1996 (TREMBLEEL O1, CHEATED)
O1-NOV-1996 (TREMBLEEL O1, LAST SEQUENCE UPDATE)
O1-NOV-1996 (TREMBLEEL O8, LAST ANNOTATION UPDATE)
PROLINE PERMEASE (FRAGMENT).
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MEDLINE; 93015751.
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                        STRAIN-S2003;
MEDLINE; 93015751
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                                                                              SEQUENCE FROM N.A.
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5: Conservative
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489 AA.
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     SELANDER R.K.;
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Pred. No. 1.8e+02;
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Fred. No. 1 8e+02
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Best Local Similarity
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EMBL: 101139: 0154298.
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SECTENCE 489 AA: "2937 MW: 69187112 CPC32;
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PPOSITE: FS00457, NA_SOLUT_SYMP_2 1.
PFAM; PF00474; SSF; 1
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P28647 rattus norv P28647 rattus norv P39533 saccharomyc QC5152 brachysholo P18837 paramecium P80396 rana rugosa P80396 rana rugosa P80396 rana rugosa P80396 rattus norv P16100 homo sapien P70386 mus musculu n19073 sus scrofa paramecium P08235 homo sapien P08235 homo sapien P08235 homo sapien P08236 atlmonalla p10502 salmonolla p10505 cocharomyc p23686 homo sapien P05622 mus musculu p244386 homo sapien p30505 homo sapien p30505 homo sapien p30505 homo sapien p30502 mus musculu p244386 homo sapien p30502 homo sapien p35029 homo 
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FRETY -> VORNH (IN REF. 1).
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TRON-SULFUR (4FE-4S)
TRON-SULFUR (4FE-4S)
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Pred. No.
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PIE: S302985: S29986:

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A HSSF: E08046: 12AA

DR PROSTITE: PS90420: TINGETE_C2H2: 3.

KW PROSTITE: PS90420: TINGETE C2H2: 3.

KW REBEAT: ZING-FINGER; METAL-BINDING.

FT DOMAIN 299 379 CING-FINGE
FT DOMAIN 299 379 C2H2-TYPE
TN.FING 329 351 C2H2-TYPE
TN.FING 329 351 C2H2-TYP
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Best Local Similarity
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OXIONY E., JOWETT T.:

NUCLEIC ACTUS RES. 21:1087-1095(1993).

--- FUNCTION: SEQUENCE SPECIFIC DNA BINDING TPANSCRIPTION FACTOR.

BINES TO INC. SECUENCE DNA SITES LOCATED IN THE PROMOTER REGION.
                                                                                                                                                                      PRAT A., KATINKA M., CARON F., MEYER E.:
J. MOL. BIOL. 189:47-60(1986).
-!- FUNCTION: THIS PROTEIN IS THE SURFACE ANTIGEN ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (REL. 13, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
01-AUG-1990 (REL. 15, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BRACHYDANIO KERIO (ZEBKAFISH) (ZEBKA DANIO).
EURARYOTA: METAPOA: OHORDATA: VERTERRATA: PISCES: ONATROSTOMATA:
OSTEICHTHYRS: ACTINOPIEWYGII: CYPRINIFORMES.
ANTIGEN OF PARAMECIUM PRIMAURELIA.

11 SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPT-ANCHOR

17 THAS INTERNAL HOMOLOGIFS AND A HIGHLY PERIODIC SCRUCTURE WITH

17 PERIODS OF ABOUT 75 RESIDUES, EACH PERIOD CONTAINING 8
                                                                                                                                                                                                                                                                                  MEDLINE; 87060934.
PRAT A., KATINKA M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARAMECIUM PRIMAURELIA.
EUKARYOTA: PROTOZOA: CILIÓPHOKA; CILIATA; HOLOTKICHA; HYMENOSTOMAIIKA
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=156
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COHO-TYPE.
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4M; 45:31375 CKC31;
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Pred. No. 66;
Mismatches
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Best Tocal
  GAE3_RANRU
P80397;
01-NCV 1395;
C1-NOV-1595;
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P80396;
01-NOV-1995
01-NOV-1995
01-NOV-1997
                                                                                                                                                                                                                                                    MEDLINE: 95:91844.

PARK 1 M 1700 1 E JEF B 1

BIOCHEM, BIDPHYS RES. COMMUN. 205:948-954(1994).

-!- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY HAS A BROAD SPECTRUM OF ACTIVITY AGAINSI BOTH GRAM POSITIVE AND GRAM NEGATIVE HACTERIA, FUNGI AND PROTOZOA.
                                          PANPI
                                                                                                                                                                                     AMPHIBIAN SKIN: ANTIBIOTIC.
                                                                                                                                                                                                            -!- SUBGUNIT: MONOMER.
-!- SUBGULITAR LOCATION- SECRETED
-- TIRSUP SEPTIFICITY, SKIN
-!- SIMILARITY- RELOWS THE EPEVIN
                                                                                                                                                                                                                                                                                                                                               ELIKVOR
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PIR; A23475; A23475.
HSSP: P05620; lINA.
                                                                                                                                                                        SEQUENCE
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SIMILAFITY: 98% TO THE ALLELIC FORM 168G PROTEIN (P17053) IN
PERIODIC STRUCTURE AND 80% IN VARIABLE DOMAIN IN THE MIDDLE (
                                                                                                                                                                                                       FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYSTEINES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPRESSION OF A PROTEIN OCCUPS AT LOW TEMPERATURES (14-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYSTEINES, EXCEPT FOR FOUR HALF PERIODS. A VARIABLE PART OF 475 RESIDUES COMPRISES 4 ALMOST IDENTICAL PERIODS IN THE MIDDLE OF
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                                                                                                                                                                        33 AA;
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(REL. 32, CREATEC)
(REL. 32, LAST SEQUENCE UPDATE)
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                               STANDARD;
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                                                                                                                      Score 26; DB 1
Pred. No. 7.3;
n. Mismatches
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Pred No 3 5e+02;
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37 X 75 AA APPROXIMATE REPEATS
88% TO FARAMECIUM TETRAURELIA /
                                                                                                                                                                        BY SIMILARITY.
96F2A97A CRC32
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Best Local :
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            JONES M.H., DAVEY P.M., APLIN H., AFFARA N.A.;
GENEMICS 29:796-800(1995).
GENEMICS 29:796-800(1995).

-I EUNCTION: INCOLVED IN SPERM-FGG ADHESION. UPON FERTILIZATION SPERM MUST FIRST PENETRATE A LAYER OF COMMULUS CELLS THAT STEPPOWNES THE FAG BEFFGEF PENCHING THE CONTAINING HYALLTRONIC COMMUNICS CELLS ARE EMBEDDED IN A MATRIX CONTAINING HYALLTRONIC ACITO WHICH IS SECHED PENCH TO CAVULATION. THIS SECHED NAIDS IN PERETFATING THE LAYER OF CUMULUS CELLS BY DIGESTING HYALLTRONIC ACID.

ACID.

ACID.

ACID.

ACITU-BETA-F-GLOTOSAMINE AND F-GLUCTERONATE RESIDUES IN CONTAINING BETA-F-GLOTOSAMINE AND F-GLUCTERONATE RESIDUES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYAI_HOMAN STANDARD; PRI; 509 AA. P88567; P88567; P98567; P99667; P99767; P997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _HUMAN
                                                                                                                                                                                                                                                                                                                                                                           FEBS
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LIN Y , KIMMEL L H ,
FROT NATE ACAP SOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EUTHERIA; PRIMATES
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EUKAFYOTA, METABOA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SPERM ADHESION MOLECULE 1). SPAM1 OR HYAL1 OR FH20.
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ETKARYSTA: MEINICA, THIELATA,
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336:545-548(1993).
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100.0%;
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A8160CBB CRC3:
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Pied. No.
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10071-10075(1993).
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CONTI BL, FIM S.C., CHUN LC., CHUN H.S., JOH T.H.;
GRIGHITED TIME 1-73 TO EMBLYCHNHANK/JOHN LAIA HANKS
FORGTE N. AND MIRITS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STEMMILATES INTERFERON GAMMA PRODUCTION IN THELPER TYPE I
                                                                                                                                                                                                                                                                      HOMO SAPIENS (HUMAN)
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TO 1900 (REC. 36) LAST ANNOTATION UPDATE)
OLEUKIG 18 FEEDIRSOK (IL-18) (INTEREEMON-GAMMA INDUCTOR PACTOR)
GAMMA GAUSSING FACTOR) (INTERLEUKIN-1 GAMMA) (IL 1 GAMMA).
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KONISOT K., MITALSHE M., FUJII M., TORIGOR
IKETA M., OKANURA H., KUKIMOTO M.;
156.1274 4279(1996).
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                                   BY SIMILARITY.
INTERLEUKIN-18.
Score.
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P -> A (IN REF. 2).
L -> W (IN REF. 2).
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Pred. No.
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N €
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DB 1;
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       Length 193;
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Best Local Similarity
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SEQUENCE
                                                                                               SIANGARD PRI 150 AA.

(19073)

(5-101-1998 (PEL 36, CREATED)

15-JUL-1998 (REL 36, LAST SEQUENCE UPDATE)

15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)

15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)

15-JUL-1998 (REL 36, LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE FROM N.A. FOSS D.L , MURTAUGH M.P.;
                                             SUS SCROFA (PIG)
EUKARYOTA, METAZOA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE: 96061009.

KAMMURA H., TSHIHI H., KUMATSU I., YUISUDO M., HAKUFA A.,

TANAMURA H., TSHIHI H., KUMATSU I., YUISUDO M., HARTORI K.,

TANABOR T., TORIGOE K., OKURA T., NUKADA Y., HATTORI K.,

AKITA K., NAMBA M., TANABE F., KONISHI K., FUKUHA S., KURIMOTO M.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P70380;
15-JUL-1998 (REL. 36, CREATED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                   EUTHERIA;
                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:107936; IGIF.
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NOD; TISSUE=PANCREAS; MEDLINE; 97174346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-191 FROM N.A.
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EUKARYOTA: METAZOA; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTERLEUKIN-18 PRECURSOR (II-18) (INTERFEEEN-GAMMA INDUCING FACTOR)
(IFN-GAMMA-INDUCING FACTOR) (INTERFEUKIN-1 GAMMA) (IL-1 GAMMA).
                                                                   IL18 OR IGIF
                                                                              (FRAGMENT)
                                                                                      (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)
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U66244; G1561736;
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PI5109:
01-ADP-1900 (PEL 14 OPEATED)
01-ADP-1900 (PFI 15, LAST SEQUENCE IPDIATE)
01-NOV-1997 (PFI 35, LAST ANNOTATION UPDIATE)
01-NOV-1997 (PFI 35, LAST ANNOTATION UPDIATE)
0-SELECTIN PRECURSOR (CRANDIF MEMBRANE PROTETN 140) (GMP-140) (PADGEM)
NT62F; (LEM5-7) LE ENCLIHEITAL CELL ACHESION MCLECULE 5) (LEMM3).
SELP OR GMRP:
HOMO SAPINES (HUMAN)
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MEDLINE: 97152062.

MEDLINE: 97152062.

TINTI C., SON J.H., TOH T.H.;

J. BYOL CHEM. 27252075.2037(1987)

-1- FUNCTION: AUTMENTS NATURAL WITLES TELL ACTIVITY IN SPLEEN CELLS
AND STIMULATES INTESERFON GAMMA PRODUCTION IN T. HELPER TYPE I
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-:- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND STREMILATES INTERFERON GAMMA PROPORTION IN THELPER TYPE I
CELLS (BY SIMILARITY).
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EURARUUTA METATUA, THURUTATA, VERTERRAIA, LEIRARULA, MAMMALIA.
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Pred. No.
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PS003ITE: PS000518; C_TYPE_LHOTIN_1; 1
PS003ITE: PS00041; C_TYPE_LECTIN_2; 1.
CELL ADBESION: TPANSMEMBRANE: GTYPOPROTEIN:
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PROTEIN SCI 2:1799-1810(2)
-1- FUNCTION: CA(2+)-FFPENTENT RECEPTOR FOR MYELOID
10 CARROHYDRAIES...N NEUTROPHIIS AND MONOCYTES. T
RECOGNIZED IS STALYL-LEWIS X.
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p44650:
01-N0Y-1995 (REL. 32, CREATED)
01-NOY-1995 (REL. 32, LAST SEQUENCE UPI
01-NOY-1995 (REL. 32, LAST ANNOTATION (
FERFEDOXIN TYPE PROTEIN NAPF HOWOLOG.
NAPF OR HIG342.
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PROSITE: PSOOI
ELECTRON FRANS
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KERLAVAGF A P. BUIT C T. TOMR J P. DOUGHERTY B.A. MERRICK J.P.
MCKENNEY K. SUITTON G. FITTHUGH W. FIELDS C.A. GOCAYNE J.D.,
SCOTT J D. SHIRLEY R. LIU L.-I. GLODEK A. KELLEY J.M.,
WEIDMAN J.F. PHILLIPS C.A., SPRIGGS T. HERBLOM E. C. CTTON M.D.,
UTTEFRACK T P. HANNA M C. NGUYEN D T. SAUDEK D. M., HARNDON B.C.
EINE L.D., FRITCHMAN J I. FUHRMANN T D. GEOGHADEN N.S.M.,
GNEHM C.L. MCLUNALD L.A. SMALL K.V., FRASER C.M., SMITH H.O.,
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-1- SIMILARIY: REFLONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
EMBL; M16801; G307166; -.
PIR: A29513: A29513.
                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32719; G1573313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENTER J.C.;
SCIENCE 269:496-512(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIINE: 95350630;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAEMOPHILUS INFLUENZAE.
PROKARYOTA: GEACILICUIES:
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HSSP; P06536; 1GDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- FUNCTION: INVOLVED IN ELECTRON TRANSFER 'H-SIMILARITY: THE IFON-SULFUR CENTERS ARE BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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5: Conserv
                                                                                                                                                                                                                                                                                                                             PSOO198; 4FE4S_FEPREDOXIN; 4FE4S_FEPREDOXIN;
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32, LAST SEQUENCE UPDATE)
32, LAST ANNOTATION UPDATE)
                                11-NN-SULFUR: 4FE-4S.
48 160N-SULFUR 1
150 160N-SULFUR 1
150 160N-SULFUR 1
150 160N-SULFUR 2
23 160N-SULFUR 2
25 160N-SULFUR 2
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8 1 (4FE 48)

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8 1 (4FE 48)

18 2 (4FE 48)
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1.4e÷02;
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                                                                 Y SIMILARITY)
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STATE SECTION OF SECTI
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The Address To Conserve
Search completed: June 22, 1999, 10.59:46
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22 SUBMITTED (FEB-1996) TO EMBL/GENANK/IDAD DATA BANKS.

23 SUBMITTED (FEB-1996) TO EMBL/GENANK/IDAD DATA BANKS.

24 SUBMITTED (FEB-1996) TO EMBL/GENANK/IDAD DATA BANKS.

25 SUBMITTED (FEB-1996) TO DAY APPLICATION AND ESSENTIAL FOR VIABILITY.

26 C. SERVELLITY AP LOCATION: NUCLEAR (POTENTIAL).

27 C. SERVELLARITY: BELONGS TO THE MCM FAMILY.

28 EMBL: SE68467; G545211; -.

29 EMBL: Z69269; E221200; -.

20 EMBL: Z69269; E221200; -.

20 EMBL: Z69269; E221200; -.

21 EMBL: Z69269; E221200; -.

22 EMBL: Z69269; E221200; -.

26 EMBL: Z69269; E221200; -.

27 EMBL: Z69269; E221200; -.

28 EMBL: Z69269; E221200; -.

29 EMBL: Z69269; E221200; -.

20 EMBL: Z69269; E221200; -.

20 EMBL: Z69269; E221200; -.

21 EMBL: Z69269; E221200; -.

22 EMBL: Z69269; E221200; -.

23 EMBL: Z69269; E221200; -.

24 EMBL: Z69269; E221200; -.

25 EMBL: Z69269; E221200; -.

26 EMBL: Z69269; E221200; -.

26 EMBL: Z69269; E221200; -.

26 EMBL: Z69269; E221200; -.

27 EMBL: Z69469; E221200; -.

28 EMBL: Z69469; E221200; -.

29 EMBL: Z69469; E221200; -.

20 EMBL: Z69469; E221200; -.

21 EMBL: Z69469; E221200; -.

22 EMBL: Z69469; E221200; -.

23 EMBL: Z69469; E221200; -.

24 EMBL: Z69469; E221200; -.

25 EMBL: Z69469; E221200; -.

26 EMBL: Z69469; E221200; -.

27 EMBL: Z69469; E221200; -.

28 EMBL: Z69469; E221200; -.

29 EMBL: Z69469; E221200; -.

20 EMBL: Z69469; E221200; -.

20 EMBL: Z69469; E221200; -.

20 EMBL: Z69469; E221200; -.

21 EMBL: Z69469; E221200; -.

22 EMBL: Z69469; E221200; -.

23 EMBL: Z69469; E221200; -.

24 EMBL: Z69469; E221200; -.

25 EMBL: Z69469; E221200; -.

26 EMBL: Z69469; E2
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P41389:
P41389:
01-0CI-1995 (REL. 32, CREATED)
01-0CI-1996 (REL. 34, LAST SEQUENCE UPDATE)
01-0CI-1996 (REL. 34, LAST ANNOFATION UPDATE)
COLL DIVISION CONTROL FROTEIN HDA4.

NDA4 OR SPACEHAPOMYCES POMBE (FISSION YEAST).
SCHIZOSACCHAPOMYCES POMBE (FISSION YEAST).
SCHIZOSACCHAPOMYCES POMBE (FISSION YEAST).
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Best Local Similarity 100.0%: Pred. No. 21; 
Matches 5; Conservative 0; Mismatches 0; Indels
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MEDLIND: 94129984.

MIYARE S. SKISHTON . SAMETIMA I , HJEASKA V . IGEA I , SAITOH I.,
YANAGIR M.:
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Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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DNA-directed RNA				69 5	44
VPS9 protein - yea		in H		70	دي ان.ا
hypothetical pro		£.			F.
maks protein - Esc	Cart	1 · · · · · · · · · · · · · · · · · · ·	(E)	. 1	gi in June
mukE protein . E		34-2		70	40

ALIGNMENTS

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Arbeterene d. A(186)
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As A 1998 as 1997 PP mR
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A.Molecule type: mRNA
A.Residues: 658-761 (RES)
A.Residues: 658-761 (RES)
A.Cross-references: GB: M23032; NID:q192391; PiD:q192392
A.Cross-references: GP: M23032; NID:q192391; FiD:q192392
A.Cross-references: GP: M23032; NID:q192391; FiD:q192392
A.Cross-references: GP: M23032; NID:q192391; Fixed by removal of four residues and alternative complement pathways 3.705 convertase.

alternative complement pathway 3.705 convertase.
C.Comment: GBa anaphylatoxic is a vasoactive peptide and a anaphylatoxic of information.
C.Comment: GBb. with its highly reactive thiol group. binds to the surface of conventase in the complement of the surface of the surface of conventase.
C.Comment: GBb. with its highly reactive thiol group. binds to the surface of conventase of this plasma protein is the liver. Superiamity alpha 2-macroglobulin
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A:Molecule type: protein
A:Molecule type: protein
A:Residues: 671-677,'X',679-680 <SA2>
A:Residues: 671-677,'X',679-680 <SA2>
R:Féy, G.: Eumdey, H.: Wiebauer, A.: Whitehead, A.S.: Springer Semin. Immunopathol. 6, 119-147, 1983
A:Title: Structure and expression of the C3 dene.
A:Reference number: 149563; MUID:84045280
A:Auccession: 149563
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A/Regiduos, 25:380 (2),138 240 :FEXX
A/Regiduos, 25:380 (2),138 240 :FEXX
A.Dross inferences: 08.M35(f), NID.3192280, FID:4192281
R:Fey, G.H.: Wiebauer, K.: homdey, H.
Ann N. Y. Agad sqi 421, 207:312, 1983
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A:Accession: I49576
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A Criss references GB AE001322, GB AE001273, NIE g3328916, FID g3328929
A:Experimental source: serotype D, Strain UW-3/Cx
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Mol. Biocher,
A.Title Clear
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Of Species: Plasmodium yoelii
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Of Accession. A45532, A45531
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A.A.D. as Majes, W.S., Berndersky, M., Karpk, P.D., Smith, B.O., Prason, O.M., Vente A.Title: The complete genome sequence of the gastric pathoger Hellochacter pylori.
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C:Species: Mus musculus (house mouse)
C:Date: 3i:Dec:1993 #sequence_revision 02-lun-1904 #*ext_riange lasop:lase
C:Accession: S15661; S19108
R:Rutherford, M.N.: Kumar, A.: Nissim, A.: Chebath, T.: Williams, B.R.S.
Nucleic Acids Res. 19, 1917-1924, 1991
A:Ittle: The murine 2 5A synthetase locus
A:Beference number: S15660; Million 19232992
A:Accession: S15661
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A:Residues: 1-175;/L;177-192 <WIL>
A:Cross-references: EMBL:x55982; NID:q49714; PID:q49715
C:Superiamily: oliqo(A) synthetase
C:Keywords: nucleotidyltransferase
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A:Residues: 1-270 <MAL
A:Cross-reference: GB:M96770; NID:g164622, FID:g1646.
C:Superfamily: interleukin-1
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A;Title: Nucleotide sequence of parcine interleukin-;
A;Reference number: 146620
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C:Species: Sus scrota demestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #revt_of man of May-1907
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Best Local Similarity
183 TURISETRI FVSAQNEDERVULKELPETRKTIKDETSILLEFWEK----HONMOVEKSAAH
                                                                                                                        11 KYNAMEVINALIUNIAFMLSIISEERSLYIMAAVIMULEAVALIMAA IIRULEÇIPV 18.
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                                                                                                                                                                                                                                                                                 Y Match 9.3%; Seere TELE, DE Local Similarity 20.6%; Pred, No. 3.8;
                                                          63 TISVKOEKI-STISCENKIISEKEM NPPDNIKETKSDIIFFQFSVPOHHMKMUFESSSY 11
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                                                                                                                                                                  * KLSVIENINIQVIETOQVINERTEEDMED----SDOETNAFFT; EIISXYEDSCHEGMAV 62
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EGYFLACURES 121

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A:Experimental source: TCO-4 cells
A:Note. segmence inconsistent with nucleotide translation
B:Chile A:Note. Segmence inconsistent Note.
A:Chile A:Note. Segmence inconsistent in M:Chile A:Note. Segmence is a submitted to the EMBL Data Library, July 1992
A:Description: A transforming gene isolated by expression cloning from Ewing's sarcome.
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A.Reference sumber. A48713; MUID:94043034
A.Reference sumber. A48713
C:Species: Gallus gallus (chicken)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 19-Dec-1997
C:Arcession: $57450
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C:Superfamily protein kinase homology
C:Keywords: alternative initiators: prote-opegene
E:136-388/lwwwain: protein kinase homology <KIN>
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A; Accession: S31639
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A:Accession, B48713
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A:Molecule type: mPNA
A:Pesidies 1:45 Ary
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A:Title: The human root proteromoregene encodes two protein scring/throoning k
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A: Residues: 1-467 /CHA>
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CiSpectes: Mycoplasma genitalium
C.Date 10:New-last asrquence_recusion 10 New-last acceptions in Septio98
C.Accession H64245
R.Frascr, C.M.: Gorayne, T.D.: White, O.: Adams, M.D.: Clayton, B.A.: Eleist R.Frascr, C.M.: Gorayne, T.D.: White, O.: Adams, M.D.: Clayton, B.A.: Eleist M.: Fuhrmann, T.: Nguyen, D.: Citterberk, T.R.: Sawdek, D.M.: Phillips, C.A.:
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R:Ohara, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
Jpn. J. Cancer Res. 84, 518-525, 1993
A:Title: The murine ont proto-concegene; genome structure
A.Beference number: 149609; MUID:93308016
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A:Molecule type. mRNA
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C:Species: Mus musculus (house mouse)
C:Sete: 02-Jul-1906 #seguence_recision
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Best Tocal Similarity 22.4
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Best Local :
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22.4%; Pre/
29;
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Illigs, C.A.: Merrick,
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Copyright (c) 1993 - 1998
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ECR 150MAN
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ILLA BOVINN
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III16_FIG
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                                                            ILL8_MOUSE SIANDARD; FRT; 192 AA.

ILL8_MOUSE SIANDARD; FRT; 192 AA.

P70380;

15-JUL-1998 (PEL 36, CREATED)

15-JUL-1998 (PEL 36, LASI SEQUENCE UPDATE)

15-JUL-1998 (PEL 36, LASI ANNOTATION UPDATE)

INTEDITYN 18 PERCURSOF (IL-18) (INTERFERON-CAMMA INTUING FACTOR)

(IFN-GAMMA INSUCING FACTOR) (INTERFERON-CAMMA INTUING FACTOR)
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TITE HUMAN

STANDARD: PRT: 193 AA.

014116:
014116:
15-001-1998 (REL. 36 CREATED)
15-001-1998 (REL. 36 LASI SENGENCE UPDATE)
15-001-1998 (REL. 36 LASI ANNOTATION UPDATE)
INTERPREUNIN-19 PRECURSOF (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
(IFN-CAMMA-INDUCING FACTOR) (INTERFERON-GAMMA INDUCING FACTOR)
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SUBMITTED (FEB-1997) TO EMEL/CENBANK/DEST DATA BANKS.
FUNDAMENTS NATURAL FULLER OF LACTIVITY IN SPITEN OF LS
AN: STIMULATES INTERFERON GAMMA PROTOCTION IN I HELEEK TIPE I
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MISHIO S., NAMBA M., OKUPA I., HATTOPI K., NUKADA Y., A TORIGO S., KONISHI K., MICALLEF M., FUJII M., TORIGOE FUKUDA S., IKEDA M., OKAMUPA H., KURIMOTO M.: J. IKEDA M., OKAMUPA H., KURIMOTO M.: J. IMMUNOL. 156:4274-4279(1996).
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HOMO SAPIEMS (HUMAN).
EURARYOTA: METAZOA: CHORLATA: VERTEBRATA: TETRAPOLA; MAMMALTA:
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EMBL; 090434; G1899242;
it18 OR IGIF.
MUS MUSCULUS
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TIN. INVEST 191454 474 (1917).
ETMOTI N. ATTMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
AND SIGNUATES INTERFERENT SAMMA FRODUCTION IN THELPER TYPE I
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Best Local Similarity 63.9%; Fred. No. 6.7e-42;
Matches 93; Conservative 29; Mismatches 27;
P18430;
01-NOV-1990 (REL. 16, CREATED)
01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPED CHAIN NON_TER SEQUENCE
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0.19073:
15-JUL-1998 (REL. 36, CREATED)
15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
INTERLEWIN-18 PROTUPESOR (IT-18) (INTERLEWIN-1 GAMMA) (IT: JAMMA)
(IEN-SAMMA-INDUCING FACTOR) (INTERLEWKIN 1 GAMMA) (IT: JAMMA)
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LUSS C.L., METAUGH M.P.:

STEMITTED (THE 1997) TO EMMILYSENBANK/19982 CAIA FANES.

STEMITTED (THE 1997) TO EMMILYSENBANK/19982 CAIA FANES.

TO EUROTION AND STANDLATES INTERFERON GAMMA PRODUCTION IN THELPER TYPE I

AND STANDLATES INTERFERON GAMMA PRODUCTION IN THELPER TYPE I
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EUKARYOTA: METAZJA: CHUPUATA: VERTEBPATA: LETRARHUA: MAMMALJA:
EUTHERTA: ARTIODACTYLA.
                                                                                                               IL1A_PIG
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IL18 OR IGIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 62.9%; Score 513; DB 1; Lenath 160; Local Similarity 76.9%; Prod. No. 2.2e-41; Indels 0: 55% of Compensation 18, Missatthes 12, Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                              39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 AVTISVKOEKISTLSOENKIISEKEMMEPENIKOTKSDIIFELWSVESH USGGEESSST 12
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Best Local :
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P04822;
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INTERESTRIVER 1 ATRHA PRECIPEOR (TEST ALCHA)
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                                                                                                                                                                                                      100 TORINGTO TYPHAGMENTATY CRECERTEXTIX DETSCHERWEX - - - HSMMDMEKSAAB
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THE SIMILARITY AMONG THE II-1 PRECUPEORS SURGESTS THAT THE AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION THE LACK OF A SPECIFIC HYDROPHOGIC SERMENT IN THE PRECUPENCY SECURENCY SUBJECT OF IS PELEASED BY DAMAGED CELLS OF IS SECRETFO BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THEE M. STAMMERA & M. MISTANISH M.F. MALITOR T.W.
MITTED MAN. 1992; IN EMELINENSAM JOED NAMES. IL-1 STIMBLAIES
EUNCTION. EROCHTER BY ACTIVATED MACHOPHAZES, IL-1 STIMBLAIES
THYMOCYTE SETTIFICATION BY INCTING II-2 RELEASE, B-CELL
MAJURATION & PROLIFERATION. & FIBROBAST GROWTH EACTOR ACTIVITY
MAJURATION & PROLIFERATION. & FIBROBAST GROWTH EACTOR ACTIVITY
IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, RETING
IL-1 PROTEINS AS ENCOGENOUS EXPOGEN, AND ARE REPORTED TO STIMULATE
THE FELFASE OF PROSTAGIANUIN AND COLLAGENASE FROM SYNOVIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91
                                                                                                                                                                                                                                                                              KISVIKNI NDEVI FIDEGANPPLFEDMID----SECPDNAPPII-FIISMYKDSEPPBMAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; P01583; 1IIA.
IIE; PS0C253; I
                                                                                                                                                       PKLFIATRQEK 249
                                                                                                                                                                                                                                                     KYNEMBVINHOOTINDAFNOSTIBDESGOYLMAAVLUNLDEAVKEDMAAYTSUDDSOLBV 180
                                                                                                                                                                              EGTELACEREN 131
                                                                                                                                                                                                                             TISVYOTY: STI SOFWYITSFYEM: WPPDNIKDTKSDIIFFOFSVFOHDNKMCFESSSY 120
                                                                                                                                                                                                                                                                                                                  Similarity
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METAFOA CHORDATA
                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              53: INTERLEUKIN_1;
                                                                                            STANDARD;
                           05. CREATED)
05. LAST SEQUENCE UPDATE)
32. LAST ANNOTATION UPDATE)
88A FFECURSOR (IL-1 ALPHA).
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112
270 P
1020 P
1441 P
245 E
255 F
20798 MK
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FOTENTIAL.
N -> I (IN)
F -> L (IN)
F -> R (IN)
F -> R (IN)
TRACTOR
                                                                                                                                                                                                                                                                                                                Score 81.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERLEUKIN-1 ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1) 1.
TYPIAMMATORY RESPONSE, FYROSEN
                                                                                                                                                                                                                                                                                                     Mismatches
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N REF 2).
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CO3_MOUSE
TO DO3_MCUSE STANDARD, PRI, 1003 AA AC p01027;
UT 21-UUL-1966 (REL, 01, CREATED)
DT 01-FEB-1996 (REL 33, LAST SPOURNCE UPDATE)
DI UL-NUV-1997 (REL, 35, LAST ANNOTATION UPDATE)
DF 01_MPLEMENT 03_PRECUBSOF (BEE-MSE) (CUNTAINS
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Best Local Similarity
Matches 91; Conser
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SEQUENCE
                                                        MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHUE M., FURUTA R., FURUI T., YAMADA M., NAKAMURA NUCLEIC ACIDS RES 13-5864-5882(1985)
                         PHILDS: IRANS. R. SOC. LOND...
                                          DOMDEY H.;
                                                                                                               EUTHERIA; RODENTIA.
                                                                                                                            FINKAPYOTA;
                                                                                                                                          MUS MUSCULUS (MOUSE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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EURAFYCIA, METALIA, ISIBLAIA, VESTEEFAIA.
SEQUENCE OF 671-1663 FROM N.A.
                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBURYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEGPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYTOKINE; MACROPHAGE;
                                                                                                                                                                                                                                                                                                                     244 IATKPE 249
                                                                                                                                                                                                                                                                                                                                                                             187
                                                                                                                                                                                                                                                                                                                                                125 LACEKE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                 127 IÉTTKOFFTUNGÁLKOSÍVEGTSGOVIFAAFGANGELAVKILMSVYMISEDSILÞVILRI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                6...#
15.3
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MATURATION & PROTTERNATION, & FIREBEOGLAST GEOMETH FACTOR ACTIVITY.

TO FROTEINS ARE INVOLVED IN THE INFLAMMATCRY RESPONSE, BEING IDENTIFIED AS ENGGENOUS PYROGEN, AND ARE REPORTED TO STIMULATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUNTT MANAMER.

THE FINITARITY ANIMO THE LL PRECURSORS SUGGESTS THAT THE ANIMO ENUS OF THREE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

THE LACK IF A SITIIFIT HYDEOLHORIC SEGMENT IN THE PRECURSOR SECRETIFITS BY DAMAGED CELLS OR IS SECRETIFIT BY A MECHANISM CIFFERING FROM THAT USED FOR OTHER SECRETIFITS AN A MECHANISM CIFFERING FROM THAT USED FOR OTHER SECRETIFITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE RELEASE OF EROSTAGLANDIN AND COLLAGENASE FROM SYMPUTAL CELLS
                                                                                                                                                                                                                                                                                                                                                                            SOTELEVSAONEDEDALLKEMBETERITIESESETEFFWET---GONKNYFKSAANFOLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFWINIQUIFINGONFILLEDMILSECRONAFRII----FIISMIKDSQFRGMAVIISV 66
                                                                                                                                                                                                                                                                                                                                                                                                      ** TERRISTISCIESELISCEEM** WEST WINDIESELIESE LIEU LISVEGUUNEMARTESUSTEGNE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P01583; 1ITA.
PE; PSC0253; INTERLEUKIN_1;
                                                     85038854.
                                                                                   FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
199
141
267 M.:
                                                                                                                              METAZOA: CHORDATA:
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POTENTIAL.
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POTENTIAL.
4468A196 CEC22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fred. No. 1;
                                                      E.A.,
                                                                                                                            VERTERRATA; TETRAPODA.
                           'n.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFLAMMATORY RESPONSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                           BloL.
                                                     TACK B.F..
                                                                                                                                                                                  UPDATE)
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                           SOI.
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                           306:533-344(1984)
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                                                                                                                                                                       CHA AMARHYLATOMIN)
                                                      DE BRUIJN M.H.L.
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"BUN TO THE PROTUSSES IS EIRST PROCESSED BY THE REMOVAL OF 4 ARG
PESTITUES FROMING TWO CHAINS, HETA 4 ALPHA, LINKED BY A DISULFIDE
R ND. TO THURSTASE ACTIVATES TO BY OTPAVING THE ALPHA CHAIN,
BILEAL HI TA ANAPHYLATOXIN 4 TENERATING C3B (BETA CHAIN + ALPHA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE CINCL N. THAY'S A TENTHAL FOLE IN THE ACTIVATION OF THE MAPPENDING TO THE MAPPENDING TO THE SERVING BY CALCIUM CHERRASE IS THE CENTRAL FRACT N. IN FORTH CLASSICAL AND ALTERNATIVE COMPLEMENT PARHWAYS. ACTER A TIVALION CREEK CAN HIND COVALENTLY, VIA ITS REACTIVE HINDER ACCIVE CHARLES OF IMMUNE AGGREGATES.

THOUSE BE, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.

THOUGH A THE TEACH OF THE ACTE OF THE COMPLEMENT CS.

TA ACADEPIA FORM IS A MEDIATOR OF LOCAL INCLAMMATORY PROCESS. IT HOUSE A THE THRATTEN OF EXPLEMENT CS.

THOUGH A THE THRATTEN OF SMOOTH MUSCILE, INCREASES VASCULAR FRADERICALIST AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND FASOFIELD SHOWN THESE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WILL STATE OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . B. I.
NIVII.
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                                                                                                                                                                                                                                                                                                                                                                                        19947: ALPHA ZEROW
19917: ANAPHYLATOXIN_1; 1.
19917: ANAPHYLATOXIN_2; 1.
19918: ANAPHYLATOXIN_2; 1.
19918: ANAPHYLATOXINE; ALLERWAIE PALHWAY; PLASMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N. TOWNALL ALL DAVIDSON FL. GIBSON TL. TACK B.F., FEY G.B. THEM. 1894 (1845)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FARTHER SPEED IN TWO PASSITIONS BY FACTOR I AND A COFACTOR IN TO A COFACTOR AND CASE WHICH IS RELEASED.

THE COMMINITARIES PROSMED CONTROL PROGRAMMENTS SUCH AS COD OR CONTROL PHASES PROSMED CONTROL PRAGMENTS SUCH AS COD OR CONTROL PHASE PRAGMENTS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE: NEATHS I ANAPHYLATOXIN-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOTAL STEERS A. PRINT TORIGHAR)
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                                                                                            COMMENSATION OF STREET
CLEAVAGE (BY C3 CONVERTASE)
CLEAVAGE (BY FACTOR I).
CLEAVAGE (BY FACTOR I).
                                                                                            CRE FRAGMENT
                                                                                                                                                                                                                      CRB (ALPHA' CHAIN).
                                                                                                                                                              CRG FRAGMENT
                                                                                                                                                                                        " RDG FRAGMENT
                                                                                                                                                                                                                                                                                                                   OMPLEMENT C3, BETA CHAIN.

OMPLEMENT C3, ALPHA CHAIN.
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Best Lemal Ein:
Matches 26,
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                MSP1_PLAYO STANDARD: PRI; 1772 AA. PJ3828; 01-JAN-1990 (REL. 13, CREATED) 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE) 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE) MEF 07111 STREAT PROJECT | TEETURE & MEFOODETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
DISULFID
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            CARBOHYD
                                                                                    EMBL: JU3512: G150579: -.
EMBL: J04668: G160493: -.
PIR: A28121: A28121.
PIR: A45532: A45532.
                                                                                                                                                                        BURNS J.M. JR., DALY T.M., VAIDYA A.B., LONG C.A.:

PROC NATE ACAD SCI II S A 85-602-606(1988).

-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A 1PT-ANCHOR
                        CARBOHYD
                                           CHAIN
                                                     SIGNAL
                                                                                                                                                                                                         STRAIN=17XL;
MEDLINE; 88124889
                                                                                                                                                                                                                                                               MEDIINE: 90205979
LEWIS A.P.;
                                CARBOHYD
                                                                                                                                                                                                                                                                                                         PLASMODIUM BERGHEI YOELII.
PUKARYOTA, PROTOZOA, APISYMPIEXA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
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                                                                 TRANSMEMBRANE;
                                                                           MALARIA; MEROZOITE; POLYPROTEIN; REPEAT; SIGNAL: GLYCTGROTEIN
                                                                                                                                                                                                                               SEQUENCE OF 1093-1772 FROM N.A.
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                         (PMMSA) (230 KD).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              447 SIMHNSNNYLHISVSRMELKPGÜNL----NVNEHLRIDPGHEAKIRY 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      387 KVI.VVTQGSNAKALTQDDGVAKI.SINTPNSPQPLTITVRTKKOTLPESFQATKTMEAHPY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 QVI FITGGN - - RPI.FPI MITUSUS KINAPRI - - - - IE11SMYRISSS PROMAVITIS VEGET [ ] )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 SIESCENKI----ISEKEMNERUNIKUIKSELIEFGREVEGHUNKMOF 115
                                                                                                                             PTM. MEPOZOTTE SUFFACE ANTIGEN CONTAIN THE SEQUENCE OF BY END AND 19 KD ANTIGENS WHICH ARE THE MAJOR SCREACE ANTIGENS MEPOZOTTES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                (FUTENTIAL)
                                                                                                                                                                                                                                                    BIOCHEM. PARASITOL. 39:285-288(1990)
                                                                                                                                                                                                                                                              A.P.
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STRAIN CETELS WITCH.
KEDLINE, 9378815
OBARA R. MINCSHI J., ACKI M., TOYOSHIMA K.,
JTN. J. CANCER RES. 44.518.525(1993).
TI CANCER RES. 84.518.525(1993).
TI CONTROL PROBABLE FOLE IN SIGNAL IPANSPUCTION.
SUBSTILLULAR LOCATION CYTOPLASMIC SURMANDIRULAR GIAND, THYMUS.
TISSUE SPECIFFOTY: HIGH IN ADDICT SURMANDIRULAR GIAND, THYMUS.
SILLEM AND NEWFORM PIGESTIVE IFACT
TO PIN AUTOPROSPICATED (BY SIMILARITY) SUMAINS OF SERVING.
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-FEB-1995 (FEL 31, LAST SEQUENCE UPDATE)
-FEB-1996 (FEL 31, LAST ANNOTATION THEATE)
TERETION ON THE STRINGTHEF MINE PROTEIN KINASE (EC. 2
-CCT) (TANTER OSAKA THYRDIL EMODGENE).
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D, Mismatches
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E. Mismatches
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OF TISSUE SPECIFICITY SYNTHESIZED BY ENDOTHELIAL CELLS AND ENDOTHELIAN CELLS AND ENDOTHELI
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15-JUL-1998
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DOMAIN
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PROSITE: PS0022: EGE_1: 1.
PROSITE: PS01186: EGE_2: 1.
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EUKAPYOTA: METAZOA: CHOPDATA: VERTERRATA: TETRAPODA: MAMMALIA:
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(REL. 36, LAST SEQUENCE UPDATE)
(REL. 36, LAST ANNOTATION OPDATE)
CELL MULTIMERIN PRECURSOR.
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    AND SECUENCE OF SEX-375
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                                                                                                                                                                                                                                                                                                                                                  NOTE THAT IN WHITE OF ADAMS MID., CLAYFON E.A., NOTE OF HULL STANDARD AS SUITON OF KELLEY I MELTINAN SITE SMALL K.V. SANDUSKY M. FUHRMANN J.L. SANDUSKY M. FUHRMANN J.L. SANDUSKY M. FUHRMANN J.L. SANDERFY B.A., HOTE K.D., HULL DOCTO A. MEPPIOF THE SMORRERY B.A., HOTE K.D., HULL DOCTOR T.S., N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C.;
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4. LAST SECTENCE UPDATE)
8. LAST ANNOTATION UPDATE)
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Pred. No. 25;
Shr Mismatches 47;
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HYPOTHETICAL PROTEIN: TRANSMEMBRANE.
TRANSMEM 695 715 POTENT:
COMELICT 425 428 LEFT 15
SPOTENCE 728 AA: 96230 MW; E551
                                                                                                                                 EPASER C.M. GOCAVNE J.D., WHITE O., ADAMS M.D. CLAYTON R.A., ELEISCHMANN R.D., RUIT O.T., KEELAVAGE A.B., SUTTON G., KEELAVY J.M., FELEISCHMAN, J.L., WELDMAN, J.E., SANDLEY W.B., ETHEMANN J.L., WELDMAN, J.E., SANDLEY W.B., PHILLIPS C.A., MERRICK J.M., NGUYEN D.T., UTTERBACK T.R., SAUDEK D.M., PHILLIPS C.A., MERRICK J.M., TOMB J.-F., DOCCHEPTY B.A., BOTT K.F., HU B.-C., LUCILE T.S., PETERSON S.N., SMITH H.O., HUTCHISON C.A. III, VENTER J.C., SCIENCE 270:397-403(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (REL. 33, CREALED)
01-FEB-1996 (REL. 33, LAST SEQ
01-NCV-1997 (EEL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. SIFAIN-AIDD 13550 , G U7; MEDLINE; 96026346.
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MYCOPLASMA GENITALIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                             MYCOPLASMATACEAE.
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                                                                                                                         TRANSMEM
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                                         / Match
Local Similarity 21 9%;
14 NUNEQVERTOQGNEEDRED--MIDSECRENAPRIFILSMYKESQPROMAVIISVECES- 71
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                            32; Mismatches
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RESULT 14
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01-NOV-1988
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1. SUBSELLULAR LOCALION: ASSOCIATES WITH KINETOCHORES DURING CONGRESSION, PELOCATES TO THE SPINDLE MIDZONE AT ANAPHASE, AN OCANITITATIVELY DISCARPED AT THE END OF THE CELL DIVISION SITUATION OF SIMILABITY: BELONGS TO THE KINESIN-LIKE PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                               1026
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PROSITE: PS9069: KINESIN_MOTOR_DOMAIN2: 1.
MOTOR_DP71F1N: GERT DIVISION: AIF-HINDING: COTTED COTT: KITOSIS:
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EMBO J. 14:918-926(1995).
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G-746-799(1992)
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26, LASI SEQUENCE UPDATE)
32, LASI ANNOTATION UPTATE)
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MK. FALEFORT CHOSE.
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Pred. No. 68,
35, Mismutches
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Best Local
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-!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO, EMUS OF THESE PROJEINS SERVE SOME AS YET UNDERINE FUNCTION.
-!- THE LACK OF A SPECIFIC HYCHOPHOBIC SEGMENT IN THE PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OF IS SECURED BY MACHANISM EIFFERING FROM THAT USED FOR OTHER
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1988 (FEL. 09, LASI SEGURACE OPDATE)
01-MOY-1998 (PEL. 32, LAST ANNOTATION OPDATE)
THIERLEUKIN 1 ALCHA EMECURALE (II-1 ALCHA).
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PF0SITE, PS00000; INTESLEURIN_1
CYTOKINE: MACROPHAGE; MITOSEN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SIMILAPITY: BELONGS TO THE IL-1 FAMILY.

EMBL: M36192: G163227: -.

EMBL: X12497: G445: -.

EMBL: M37210: G163199: -.
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STILLS S., CEPREIII U.P.)
MGL. IMMUN. (5-A2Y-447)(1988)
-1- PUNCTION: BRODUCED BY ACTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDIINE; 88318652. MALISZEWSKI C.E.,
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PIR; S01379; S01379.
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ARNOTA, METATOA, CHURCAIA, VERTERFAIA, IFUSAFUTA MAGUALIA:
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                                                                                                                                                                                                                                                                                                                                         EGYFLACEKER 131
                                                                                                                                                           HUMAN
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27: Conservative
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ETRAPEATA: MEGAZIA: HUMANATA: VERTEBRATA: TETRAPODA: MAMMALTA:
PTUHERTA: TROMATER:
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A KELWAN ASTRONAN IN MIYOSHI J., TOYOSHIMA K.:

A KELWAN ASTRONAN IN MIYOSHI J., TOYOSHIMA K.:

A KELWAN ASTRONAN IN MIYOSHI J., TOYOSHIMA K.:

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BOURKE P.F., HOUT F.F., SHTHEPLANDER J., KEMP K.J.;

BOURKE P.F., HOUT F.F., SHTHEPLANDER J., KEMP K.J.;

"Discuption of a novel open reading frame of plasmodium talciparum chromosome 9 by subtelomeric and internal deletions can load to lose thromosome of cytoadherence.";

of maintenance of cytoadherence.";

MOI PROFERM, PAPASITOL 82:25-26(1996).

EMBL, X95373; E249573; -.
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01-NOV-1996 (TREMBLREL 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL 08, LAST ANNOTATION UPTATE)
NOVEL OFF ON CHROMOSOME 9 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-972H-;
WOOD V. RAJANDREAM M.A., BARBELL B.G., SKELTON J.,
SUBMITTED (MAR-1997) TO EMBL/GENRANK/DUBJ DAIN HANKS
EMBL; ALOCOCTO, Eloch446; -.
HYPOTHETICAL PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPBC3B9.02C.
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
EUKAFYOTA: FUNCT: ASSUMPTOTA: ABUTHASYOMYTETES:
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01-JUN-1998 (TREMBURE) 06 LAST SECUENCE UPDATE)
01-JUN-1998 (TREMBURE) 06, LAST ANNOTATION UPDATE)
HYPOTHETICAL 44.2 KD PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLASMODIUM FALCIPARUM.
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                               111 NKMOFESSSYEGYFLACEKERDLFKLILKKEDELGD 146
                                                                                                           220 VSEKILDGENEHLIKHTYYNNADITENETHNILLNKMYPIKEINNHHHLVEKYÇKKVEDH
                                                                                                                                                                                                                                                              192 FIQEYNKKPEEDVONPGLLNNEKSDIYEIGIY------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 EGYFUACEKERDLFKLILKKEDELGDRS 148
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                                                                                                                                                                                                                                                                                                                                          21 FIRMONDELEERMIDSIGERNAPETITITISMEERSGERGMAV... VEGEE 1.1. 1.1. CLINK. H
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                                                                                                                                                                                       ISFKEMNPPDN--IKDT---KSD1IF------
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                                                                                                                                                                                                                                                                                                                                                                                                                  ch 10.0%; Score 81.5; DB 3; 1 31milarit; 22.4%; Pred. No. 13; 35; Conservative 23; Mismatches 41:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44214 MW, 54898565 CEC52:
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Db

287

--EKMEKALKEGIVLDEDYVRENSENNLKKIMTLLD 320

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EMBL: AECO1322: G3328
SEQUENCE 856 AA: 9
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084500;
01-NOV-1998
01-NOV-1998
01-NOV-1998
                                                                                                                                                                                                                                                                                                               090681 PRELIMINARY: PRI: 2470 AA. 090681;
0290681;
01-NOV-1906 (THEMBLEEL 01 CREATED)
01-NOV-1908 (THEMBLEEL 08, LAST ANNOTATION UPDATE)
01-NOV-1908 (THEMBLEEL 08, LAST ANNOTATION UPDATE)
01-NOV-1908 (THEMBLEEL 08, LAST ANNOTATION UPDATE)
03-LOU-1MCGFFMCSHI MANNIST-6-FHOSTHATE PROFEROF,
SALLUS 346103 (CHICKEN)
CHICKEN VERTEBBATA; ARTHOGAUP
ZHOU M., MA Z., SLY W.S.;

"Clouded and expression of the dDNA of chicken cation independent mannose 6 phosphate receptor.";

PECT INT. ACAL SCI U.S.A 32 9762-9766(1995).

EMBL: U35037; G1019119; -.

PEAM: PE00040; ff02: 1.

PEAM: PE00040; ff02: 1.

EXAL SEQUIDED: $470 AA. 276445 MW. 60B68F76 CETS2.
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                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDITNE 96003859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MITCHELL W P
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BAGTERIA: CHLAMYDIALES: CHLAMYDIAGEAE;
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                                                                                                                                                                                                                                                                                         GALLIFORMES; PHASIANIDAE; PHASIANINAE; GALLUS
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AA: 96583 MW:
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26.48:
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TATUSOV
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Pred. No 23;
CC Mismatches
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LAST SEQUENCE UPDATE)
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NATURE 388:539:547(197).
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N. V. 19 (TERMELREL, OR. LAST ANNOTATION UPDATE)

N. M. OABA, DOS. (HERSEL)

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ACHOUSE COURSEN T., COODER J., COULSON A., CRAXTON M.,
COUNNELL M., COURSEY T., COODER J., COULSON A., CRAXTON M.,
COUNTY C., COURSEN C., COURSEN C., CARTMER A., GREEN F.
HILLER M., LIEF M., JOHNSTON L., JONES M., KERSHAW J.,
AND CLER M., LAIRBUILLE F., LIGHTNING T., LICYD C.,
AND CLER M., CARROLLE F., LIGHTNING T., LICYD C.,
AND CLER M., CARROLLE F., CHOWNKEEN F., SMALCON N., SMITH A.
THIERRY-MIEG J., THOMAS K.,
THIERRY-MIEG J., THOMAS K.,
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01-MAY-1997 (TREMBLREL, 03, CREATED)
01-MAY-1997 (TREMBLREL, 03, LAST SEQUENCE UPDATE)
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01-NOV-1996 (IREMBLREL, UL. LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
ONLORE (FRAGMENT).
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"Molecular cloning of equine interleukin-1 alpha and -beta cunas.": vel. immunot. immunotatict. 48:221-23:(1995).
EMBL: D42146; G1197798; -.
PROSITE: P800258; INTERLEUKIN-1; 1.
PFAM: PP00340: interleukin-1; 1.
SEQUENCE 270 AA; 40806 MW: 11246092 (MC32):
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SEQUENCE 1251 AA; 1
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MECH. DEV. 43:159-173(1993).
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EUVAFY TA, METACJA, CHURGATA, VERTEMBATA, ARCHURAURIA: AVERI
NEUGNATHAE, GALLIFURMES: PHASTANIDAE: PHASTANINAE, CA, ROTA.
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                                                                                                                                                                                                                                                                                                                              758 QUKÇALELDIĞÇAKKERDIAKVÇITSIS--SEKSYEFKIMEE 797
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hos 29; Conservative
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                                                                                                                             PRELIMINARY:
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23.5%: Pred. No. 66;
variore 47. Xismatches 64. Lideli. 23. Gaps
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22.3%; Pred. No. 10;
ative 29; Mismatches 6);
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WALERSTON R.:
STRYTTTED (FET-1445) I. EMELINENHANK/UURU DAIA RANKS
STRYTTTED (FET-1445) I. EMELINENHANK/UURU DAIA RANKS
SMBL: U80836: GITOT142: ".
PEAM: PEOCOCT /F:CRHC4: I
SECTRYTE ICT AJ. 4PIC: MW. PCTTREBB GEC31.
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CTAR S. T. T. TUEFRIN F. FAVEILLA A. FULTON L. GAPDNER A., GRENHAM T. MINISTER N. LAIREILLE P. LIGHTUNG J., LLOYD C.,
MCNUTRAY A. MARTHMARE P. O'COLLAGHAM M., PARSONS J., PERCY C.,
MCNUTRAY A. MARTHMARE P. O'COLLAGHAM M., PARSONS J., PERCY C.,
PITKEN L. POOPPA A. SATUNDERS D. SHOWNKEEN R., SMALDON N., SMITH
BONNHAMMER E., STADEN P. SULSTON J. THERPRY MIEG J., THOMAS K.,
VAUGIAN K., WATERSON P. WATSON A., WEINSTOCK L.,
WILKINSON SPROAT J. WOHLDMAN R.;
WILKINSON SPROAT J. WOHLDMAN R.;
WILKINSON SPROAT J. WOHLDMAN R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN BRISTCL N2:
HENKHAUS J., WOHLDMANN P.;
HENKHAUS J., WOHLDMANN P.;
HENKHAUS J., WOHLDMANN P.;
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BUKARYOTA: METAGGA: NEMATODA: SECERNENTEA: PHARDITTA: RHARDITIDA;
RHABDITINA: PHARCITCIDEA: PHARCITUAE: FELUCERINAE: CAENORHARDITIS
               AFABIDOPSIS THALIANA (MOUSE-EAR CRESS).
EUKARYOTA; VIRIDIPLANTAE: CHAROPHYTA/EMBRYOPHYTA GROUP; EMBRYOPHYTA:
TRACHEOPHYTA: FUPHYLLOPHYTES, SPERMATOPHYTA; MAGNOLIOPHYTA;
EUDICCTYLEDWNS: FOSIDAD: CAFPAFALES: RPASSTCACFAF; AFABIDOPSIS
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SIMILARITY TO A C3HC4-CLASS ZINC FINGER
B0432.9.
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elegans.";
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Post Local &
Matches 34
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Mutches 36; Conservative
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ROUNSLEY S.D., KAUT. S., LIN X., KETCHUM K.A., GROSBY M.L.,

RRANDON F. S. SKES S.M., MASON T.M., KEPLAVAGE A.R., ADAMS M.D.,

SOMEPVILLE C.R., VENTER J.C.;

"Arsabidags:s thallact childreners.":

SUBMITTED (JUN-1993) IN EMBL/SEMEANK/UDBJ DATA BANKS.

EMBL: ACOUGUUS, GALLABSE; ".

SEQUENCE 6:2 AA: 18803 MM; 97E1722B GEC32;
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KMBL. ANDMOTOR 747 AA: 85157 MW: 306105F2 CRC32:
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IBACHE-PHYTA, EMHHYLA-FHYTES, SFERMATOFHYTA, MAGNALLA-ESYTA:
ETDIOCTYLECOMS, EUSILAE, CAFFARALES, BRASSICACEAE, ARMEICCTSIS
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34. Conservative
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08. LAST SEQUENCE UPDATE)
08. LAST ANNOTATION UPDATE)
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78; Pred. No. 48;
29; Mismatches [9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
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Best Local Similarity 24.3%; Pred. No. 65;
Matches 35; Conservative 24, Mismatches 57, 5.8cls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q45916;
01-NOV-1996 (THEMBLEEL, 01, CREATED)
01-NOV-1996 (TERMBLEEL, 01, LAST SEQUENCE OPDATE)
01-NOV-1998 (TERMBLEEL, 01, LAST SEQUENCE OPDATE)
01-AUG-1998 (TERMBLEEL, 07, LAST ANNOTATION UPDATE)
138KDA PROTEIN ASSOCIATED WITH BONI /C1-HAEMAGGLUTININ COMPLEX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q45916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A., POPOFF M.R.;

SUBMITTED (MAY 1992) TO EMPL/GENBANK/DOBT DATA HANKS

EMBL; X66433; G509274; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLOSTRIDIUM BOTULINUM.
BACHERIA: FIRMICHIES: BACHLUNS/MICSIBHILUM GROUD: CLOSTRIDIACEAE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Organization of the botulinum neurotoxin Cl gene and i non-toxic protein genes in Clostridium botulinum ( 468 Mol. GEN GENET 243-641-640(1994).
1078 LSLKNTDGINISSVKFKLUNIDES 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1078 LSLKNIDGINISSVKFKLINIDES 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1024 TSEFVIRNYESYLDNSYIRDSSKSLLEYNKNYQLYNYVFPETSLYE
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01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
                                                                                                                                          1024 TSEEVIENVESTLENSYIEDSSKELLEVMKWFÇLYMYVEFETSLYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-468
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                                                                   134 LILKKKDENGDKSVMFTLTNLHQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LILKKKDENGDKSVMFTLTNLHQS 157
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                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                      ** ILCSASCEQUELLIMAKESEVESTAV -TLSVKOSKMSTLSCKMKIISHEEMOPPEN-- 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                              ISISVEPILKEGI: 181-NEKNVANVSILGILSINISINILSLANKNNSIYVEBELSVILDNET 1913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HELSASSERTIELLIYMYKUSEVEGLAV--ILSVKUSKMSILSCKNKIISFEEMDPPEN---9)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., EKLUND M.W., BOQUET P., POPOFF M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                GUIT ENLOSUED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                24: Mismatches 57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score #0: DB
Pred. No. 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9; Length 1194;
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                                                                                                                                   TANDNINESY 1: 17
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                                                                                                                                                                                                                                                                                                                                                                    Q24892 PRELIMINARY; PRT; 4:4 AA.
Q24892
01-NOV-1996 (TREMBIREL 01, CREATED)
01-NOV-1996 (TREMBIREL 01, LAST SEGGENCE UPDATE)
01-NOV-1998 (TREMBIREL 08 LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBIREL 08 LAST ANNOTATION UPDATE)
01-NOV-1998 (TREMBIREL 08 LAST ANNOTATION UPDATE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                types of progenitor toxin (M and L) produced by Clostridium botalinum type p CR-16 ^{\rm m}_{\odot}
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Q53550:
Q1:NOV-1996 (TERMELEEL OL CARTEE)
Q1:NOV-1996 (TERMELEEL OL LAST SEQUENCE UPDATE)
Q1:NOV-1999 (TERMELEEL OR LAST ANNOTATION COMPONENT (FRAGMENT)).
Q1:NOV-1999 (TERMELEEL SATILLYS, ULOSTFILLUM GROUP, Q1:OSTPIDTACEAE,
Q1:NOV-1999 (TERMICUTES, SATILLYS, ULOSTFILLUM GROUP, Q1:OSTPIDTACEAE,
DOWN F.C.J. BOMSTEAD J.M., TOMLEY F.M.)

"Reject - expressions is 1 validation of reliminabilized until protein kinases in Fimeria terella and fimeria maxima.";

PARASITOLOGY 113:439-448(1996).

PARASITOLOGY 113:439-448(1996).

PRAM. PE00036. effact, 4.

PFAM. PE00036. pkinasc. 1.

NON_TER
                                                                                                                            MEDLINE;
                                                                                                                                             STRAIN-HOUGHTON:
                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                         closing of Eimeria maxima antigens that stimulate
proliferation.";
                                                                                                                                                                                                                                       BUMSTEAD J.M., DUNN P.P.J., TOMLEY F.M.; "Nitrosellulese immensibletting for ident
                                                                                                                                                                                                                                                                                      SIRAIN-HOUGHION;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N A
                                                                                                                                                                                                                                                                                                                                      EIMERIA
                                                                                                                                                                                                                                                                                                                                                   EUKARYOTA; ALVECLATA; APICOMPLEXA; COCCIDIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1078 ISLENTEGINISSVERI INIDES 1101
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                                                                                                                                                                                            CLIN. DIAGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1024 TSEEVIRNYFSYLDNSYIRDSSKSLLEYNKNYQLYNYVFPETSLYE-----VNDNNKSY 1077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 IPOSASEPQIELIIYMYKESEVEGLAV--ILSVKUSKMSILSCKNKIISFEEMDEPEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LILKKKDENGDKSVMFTLINLHQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISISVERIKUGLLIFI-NUKNVANVSITGILLSIYSINIISLVNKNNSIYVEELSVLENPI 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $80809 G:311601 -
                                                                                                                              97048698.
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1196 AA
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                                                                                                                                                                                            LAR IMMUNOL
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6 | 138717 MW
                                                                                                                                                                                          2:524-530(1995)
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                                                                                                                                                                                                                                          identification
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Best Local a
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C29092;
01-NOV-1996 (TPEMBLHEL
-1-NOV-1996 (TREMBLEEL
01-NOV-1998 (TREMBLEEL
                                                                                                                    084859
084859;
                                                              01-NOV-1998 (TREMBLEEL 08, CREATED)
01-NOV-1998 (TREMBLEEL 08, LASI SEQUENCE UPDATE)
61-NOV-1998 (TREMBLEEL 8, LASI ANNOTATION CITEAT
HYPOTHETICAL 56.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 94039070.

VANDEMRFOEKK, FITEN P., BEUKEN E., MARTENS E., VANDEMRFOEKK, OPDENAKKER G., BILLIAU A.;

"Some statomet TRA Tosttletic, expression in genetically approached partification of porcine in EUR T RICCHEM 217.45-52(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SECTENCE
                       CHLAMYDIA TRACHOMATIS.
BACTERIA; CHLAMYDIALES;
                                                                                                                                                                                                                                                                                                                                                                                     EMBL: X74568; G407900;
PROSETE: FS00253; INTERLEUKIN_1: 1.
PEAM: PE00340; interleukin-1; 1.
SEQUENTY 257 AA: 29493 MW: 055517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUS SCHOEA (PIG).
EUKAFY-TA: METAFOA. CHOPDATA: VERTERBATA:
ARTIFUATTYTA: SUIF-PMES: SUINA: SUIDAE: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VANDEPBROECK K.;
SUBMITTED (AUG-1993) TO EMBL/GENBANK/DDBJ DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TREMBUREI
INTERLEUKIN 1-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          16: 0800F-1PVTCQI=-SKNINISCVXKGETET1QCSDVDGRZVSGKG-SGKGRGVGYKTE1
                                                                                                                                                                                                                                                                                                                  bes 24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 POWERVSEPARGLIFRMIARVESMELSAKDALDHEWIKSTEVIAKDSI......nl
                                                                                                                                                                                                       221 --KNRVEFESALYFNWYISTSÇAE 242
                                                                                                                                                                                                                                 106 FGHNKMEFESSLYEGHFLACCKED 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ISSUE-LIVER;
                                                                                                                                                                                                                                                                                     53 DSEVEGLAVILSVKESKMSILSCKNK----IISFEEMDP---PENIDETOSULIFFOKRV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 DD1@SDLIFF@KRVFGHNKMEFESSLYEGHFLAG@KEDFAFKLILKKKFENGD 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 @2FREITYMYKDSEVROLA····VTLSVKDS······KMSTESOKNKIISTEEMDDDENI 91
                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                 July things will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                              (A) 0.07
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                        CHLAMYDIACEAE; CHLAMYDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CREATED)
LAST SEQUENCE UPDATE)
LAST ANNOTATION HEDATE)
                                                                                                                                                                                                                                                                                                              Score 79.5; DB 4; Fred: No. 12; DB 4; Alsmatches 25.
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Fred. No. 20:
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                  506
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A.M. 851 P.S.A. REBRECHBON (1986).
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RESOUT 12
008759
ID 008759
AC 008759
AC 008759
AC 01 M2V
CT 01 GRAPM
GS MUS MUS
AC ECUPARM
OS SCITRO
FM [1]
RP SECCEN
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Best Local Similarity 18.6
Matches 35: Conservative
                                                                                                                                                                                                                                 <u>00</u>8759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.H., CLAYTON K.A.,
LACHIGDA P., WHITE O., KETTERM F. A., TOCSCH. B., LICKEY L.K., GWHIN H.
DOUGHEBPY B., TOMP T.F., FIRTSCHANN P.D., PICHAPOSON D., PETERSON H.,
KEYLAVAGE A.P., QUACKENBUSH J., SALZBERG S., HANSON M., VAH VUGI B.,
RALMER N., ADAMS M.D., GOCAYNE T., WEIDMAN J. UTTERPACK T.,
WAITHEY L., MCCOMALE L., ACTIVAH F., LEWMAN J. SALLAND S., FUJII J.,
COTTON M.D., HOPSI K., ROBERTS K., HATCH B., SMITH H.O., VENTER J. J.,
CODDING SCHEPCE OF A Lyme disease spircchaete, Borrelia
                                       MUS MUSCULUS (MOUSE).
EUKARYUTA: METACUA, CHORDATA, VERTEBRATA, MAMMALLA, CUTHURIA, RUGERUTA:
SCIURGGNATHI: MUKIDAE: MURINAE; MUS.
                                                                                                                                           01-JUN-1998 (TREMBLEEL O1-JUN-1998 (TREMBLEEL O1-JUN-1998)
                                                                                                                       01-JUN-1998 (JEMBELEE 95. CPENTED)
01-JUN-1998 (TREMBEREL 95. LAST ANNOTATION UPDATE)
01 MOV 1999 (TERMBEREL 98. LAST ANNOTATION UPDATE)
0NCOGENIC PROTEIN-ASSOCIATED PROTEIN 66-AP (6C f.3.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UI-UUN 1598 (TREMRIFEL ON, CHEATED)
01-JUN 1698 (TREMRIFEL ON, LAST SEQUENCE UPDATE)
01-JUN 1698 (TREMRIFEL ON, LAST SEQUENCE UPDATE)
01-JUN 1698 (TREMRIFEL ON, LAST ANN-TATION UPDATE)
HYPOTHETICAL 134.4 KD PROTEIN.
  SEQUENCE FROM N.A
                                                                                                                                                                                                             008759; P97482;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATURE 390:580-586(1997).
EMBL: AE0911182: GZ688785; -.
T16R: BB0838; -.
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SPOUENCE PROM N.A.
TYLAMOC 25210 / B31;
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BACTERIA: SPIROCHAETALES; SPIROCHAETACEAE; BOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 051778;
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                                                                                                                                                                                                                                                                                                                                           637 TLKNIDOS 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 FESSLYEGH--FLACOKEDDAFKLILKKKDENGDKSVM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 SVVLEHYSDEYVNILERDRIESATEESLLNUDKUSVKEGISISTEUWNLSSEYKRTENDO 521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 PELFIATKEO 143
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                                                                                                                                                                                                                                                                                                                                                                                150 TLTNLHQS 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1146 AA: 134379 MW; 2D367D40 CRC32
                                                                                                                                                                                                                                   PRELIMINARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 78; DB 9; Lenuth 1145;
Pred. No. 90;
8; Mismatches 71; Indels 44;
                                                                                                                                                                                                                                   TO 100
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RESULT
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Best Local S
Matches 31
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COMMIN 786 885

BINDING 853 853

CONFLICT 301 301

CONFLICT 343 243

CONFLICT 460 450

CONFLICT 486 486

CONFLICT 554 486

CONFLICT 554 555

CONFLICT 554 558

CONFLICT 557 557

CONFLICT 557 558

CONFLICT 557 558
024295:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HATAKEYAMA S. JENSEN J.P., WFISSMAN A.M.:
"Subcellular localization and ubiquitin-conjugating enzyme (E2)
interactions of mammalian HECT family ubiquitin protein ligases.";
J. BIOL. CHEM. 272-15085-15092(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDITAL, STOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BEAUDET A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N A
                                                                                                                                                                            447
                                                                                                                                                                                                                                                                                                                                          14 MINEOVIEVOKROPVER--PMTPIPOSASEROTPLIIYMYKESEVRGLAVTLSVKESKMS 71
                                                                                 د<u>ـــ</u>ـر
(ب)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: INTERACTS WITH THE 66 PROTEIN OF THE CANCER-ASSOCIATED HUMAN PAPILLOMAVIKUS TYPHS 16 AND 18. THE E6/56-AP COMPLEX BINDS TO AND TAPPETS THE FTO THYPE FUNCTION FOR PROTEIN FOR URIQUITIN-MEDIATED PROTEINLYSIS 66-AP IS AN E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM AN E2 UBIQUITIN-CONJUGATING ENZYME I THE FORM OF A THIOESTEP AND THEN DIRECTLY IRANSFERS THE UBIQUITIN TO TAPPETFED SUBSTRATES.
SUBCELLULAR IOCATION: NUCLEAR AND CYTOPLASMIC AND THYMUS. SUBCELLULAR IOCATION: MOST ABUNDANT IN BRAIN, HEART AND THYMUS. TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS. AND THYMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAUTION: IT IS UNCEPTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., TRRIDE, 31847575;
MGI:105098; UBE3A.
( PECOK32, HECT; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E6-Ap ubiquitio-protein ligase (UBB3A) gene is localized within owed Angelman syndrome critical region.";
ME pes 7:368-377(1997).
                                                                                                                                                                                                                                                                                NUMBER -- - TO SET TO S
                                                                                                                                                                         TLDCFKPLISFEESINEPLNDVLEMDKDYTFF-----KVETEN---KGSFMTC
                                                                                                                                                                                                                             TEROPHELISECEM - ERPENIEE IN SULLIFFENRY FUNKMETESSINEGHELAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                           EFELIMINAFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HECT;
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ASP/GLU-RICH (ACIDIC)
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D -> E (IN PEF 2).

L -> V (IN PEF 2).

T -> S (IN PEF 2).

N -- Y (IN PEF 2).

S -> F (IN PEF 2).

G -> F (IN PEF 2).

DESCVS -- MERAFF (IN PEF 2).
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OI -> SW (IN PEF 2)

OI -> W (IN PEF 2)

PTLIG -> VYSOWH (IN PEF

IS -> NL (IN PEF 2)

II -> Q (IN PEF 2)

NV -> KE (IN PEF 2)

MW: 525010E3 CPC32:
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SADDBGG
                           FFT.
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                           86.5
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Best Local :
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068317;
01-AUG-1998
01-AUG-1998
01-NOV-1998
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01-JAN-1466 (TREMPLIED 05, LAST SEQUENCE CREATE)
01-JAN-1446 (TREMPLIED 08, LAST ANNOTATION OPDATE)
01-JOV-1498 (TREMPLIED 08, LAST ANNOTATION OPDATE)
LIPOXYGENASE.
LOXI-PS-5.
PTSUM SATIVUM (GARDEN PEA)
EUKARYOTA, VIRIDIPLIANTAE. CHARCOPHYTA, EMPRYOPHYTA GROUP, EMPRYOPHYTA;
EUKARYOTA, VIRIDIPLIANTAE. CHARCOPHYTA, FEMERYOPHYTA;
EUKARYOTA, VIRIDIPLIANTAE. CHARCOPHYTA, FEMERYOPHYTA;
EUKARYOTA, VIRIDIPLIANTAE. CHARCOPHYTA, FEMERYOPHYTA;
EUKARYOTA, VIRIDIPLIANTAE. CHARCOPHYTA, MAGNOLIOPHYTA;
ENCARES. SPERMATUCHYTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBMITTED (NOV-1997) TO EMBL/GENBANK/DDBJ EMBL; Y15410; E1172502; PROSITE; PSO0081; LIPOXYGENASE_2; 1. PROSITE; PSO0711; LIPOXYGENASE_1; 1. PFAM; PFU03U5; LIPOXYGENASE; 1. SEQUENCE 866 AA; 97748 MW. GFORFSIT GE
                                                                                                                                     LEE S H. ANSELICATION M.J. MEKALANUS J.J.
"Nucleocitide Sequence and Spatiotemporally
cholorae vieSAB genes during infection.";
packets 180.3239.3.239.0.
EMBL AF031552 G312390. -
SEPTENTE 1145 AA. 129484 MW. D35FD336
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=06709-1, EL TOR;
MEDLINE; 98233722.
LEE S H , ANGELICHTO M J
                                                                                                                                                                                                                                                                                                 BACTEPIA; PROTEORACTERIA; GAMMA SUBDIVISION; VIBRIONACEAE; VIBRIO
                                                                                                                                                                                                                                                                                                                   VIBRIO CHOLERAE
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13.
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                           31 EMTETEOSASEP-OTREI---IYMYKDSEVRGLAVTLSVKESKMSILSCKNKIISFBEMD 86
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A;Cross references. EMBL.M72716, NID.q171194, PID.q171195
A;Bostani, [1]. 30911-02104, M.; 30caria, F.; Kilma, K.; Fruschi, [27].
Submitted to the EMBL Data Library, September 1995
A;Description: The sequence analysis of a 7.9 kb DNA fragment from the left
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A: Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: S62051
A;Accession: S62055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Mclecule Type: DNA
A; Residues: 1-281 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross:references. EMBL.272712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: S61128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ive new genes.
                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 36;
312 YLTVKIWDVNMDNKPLKTI-NIHE 334
                                                          133 KLILKKKDENGDKSVMFTLTNLHQ 156
                                                                                                                        268 L-CDNKTKTFEEYLDPINHN-----FFTEITSSISDIKFSPN---GPYIASED----
                                                                                                                                                                                                                                                    217 DIPDOSENIADIKETUMEETTEATTSAEEHFGEGNLEMASSSE - CITTETOMAKONS 250
                                                                                                                                                                                                                                                                                                                     14 NINDQVI-FVDKRQPVEFDMTDIDQSASEPQTPITIYMYKDSFVEGLAVTLSVEDSEMST 72
                                                                                                                                                                                      73 LSCKNKILSFEEMDPPENIDDIGSDLIFFGKRVPGHNKMEFESSLYEGHFLACGKEDDAF 3/42
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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25.0%; Fred. NO. 4.7;
ative 29; Mismatches 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lengto 526
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RESULT 5

JO1467

JO1467

JO1467

Loxin, nontoxic component - Clostridium botulinum phage (type 0)

C. Spenies: classifidium betulinum phage

C. Spenies: classifidium betulinum phage

C. Spenies: dissipidium betulinum phage

R. Fulli, N. Yokosawa, N. Fulumu, E. Billing (m. Spenies)

Bille The Langlett Harling (m. Yokosawa, N. Fulumu, E. Billing (m. Spenies)

A. Fille The Langlett Harling (m. Yokosawa, N. Fulumu, E. Billing (m. Spenies)

A. Feference number: JO1467; Mulp-42241894

A. Reference number: JO1467; Mulp-42241894

A. Residues: 1-1196 CISUs

A. Foression: JO1467 Control of the made duding for the discount A. Portoss references: EMBI-X62480; NID-4558175; FID-440489

A. Accession: P00237
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nothema

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botulinum neurotoxin associated protein ANTP-139 - Clostridium motulinum phage iC (stra NaIternate names: ANTP-139 protein C Species - Clostridium lotulinum phage iC Aspecies - Clostridium lotulinum phage iC Asyariety strain G 468 C:Date: 19-Mar-1997 *sequence_revision Of-Jun-1997 *text_change l0-Sep-1997 C:Date: 19-Mar-1997 *sequence_revision Of-Jun-1997 *sequence_revision Of-Ju
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AsPesilies, 1:20 TED:
C:Comment: This nontoxic component is a constituent of 168(500K) toxin with two other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Cruas references. EMBL.X72793. NID:g516171, PID:g516174
A:Experimental source strain 0 468
A:Note: the nucleotide sequence was submitted to the nucleotide.
                                            ArTitle: Gene seguence, cDNA construction, expression in Escherichia coli and genetical
A:Reference number: $38373
A:Accession: $38373
                                                                                                                                                                                                                                                                                  Interleukin-1 beta precursor - plg
CrSperies Sus scrofa domestica (demestic plg)
Crsater 20-bay-1994 #sequence_revision Ol-bec-1995 #text_change 08-Sep-1997
Crachession 83877
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A; Residues: 1:1196 H
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A,Addession: $46430
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A; Status: preliminary
                                                                                                                                                                                     R:Vandenbroeck, K., Eiten, P., Ber
Eur. J. Biochem, 217, 45-52, 1995
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Best Local Similarity 24.3

Matches 30, Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 LILKEKDENGDESVMETLINGEQS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WITH HUMANNESS THE STEED MAKE SEVER STAN THE SYKESKMIST SAKKKI I SKEEDMOESEN THE SEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the nucleotide sequence was submitted to the EMBL Data Library, May 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35, Consert
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24.3%;
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D4.3%, Fred. No. 14,
attive 24, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -TUDIOSULIEFOKRVPGHNKMEFESSLYEGHFLAGOKEDDAFK 133
                                                                                                                                                                                                                                      Beuken, E.; Martens, E.; Janssen, A.; van Damme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 80; DB; Pred: No. 14; 24; Mismatches
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Ribult, G.J., White, O., Olsen, G.J., Zhou, D., Eleisohmann, E.D., Sutton, G.G., Blak F. Reich, G.J., Overbeek, P.: Kirkpess, E.F.; Weinstock, K.G., Merrick, J.M., Glodek, rson, M.D., Sadow, P.W., Hanne, M.O., Gouton, M.D., Roberts, K.M., Hurst, M.A.: Kaine Science 273, 1058-1073, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C, Genetics.
A: Map position. FGR733017:732530
                                                                                                                                                                              C:Accession: 0714
F:Stephens, F S.:
                                                                                                                                                                                                                            hypothetical protoin 31971—Thlumpila trade matis (our 19go I. Kitalo TWA)TX:
C:Species: Chlamydia trachomatis
C:Date: 13:Sep:1948 #sequence_revision 13-Sep:1948 #fext_clungs 13-Sop-1948
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A;Title: Complete genume sequence of the methanogenic archaeon, Methanogocous jannaso
A;Reference number: A64200: MUTD-96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C:Species: Methanococcus jannaschii
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A, Molecule type...
A, Residons 1-106
                                                                         A;Reference number, A71460
A;Accession: D71461
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A, Residues: 1-167 <BUL>
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                                                 A:Status: preliminary
                                                                                                                             Altesoription Genome sequence of an obligate intracellular pathogen of humans: Chlam
                                                                                                                                                        submitted to GenBank, May 1998
                                                                                                                                                                                                                                                                                                                                            RESULT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98 PLSSHD1------EELNKKLIEB-----VKYIKITFAELFEH--FKVLLETK 136
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A; Authors: Venter, J.C.
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Peterson, J.: Kerlayage, A.R.: Quackenbush, J.: Salzberg, S.: Hauson, M.:
n. 7 - Parijard, S.: Pujlij, P.: Potton, M.D.: Horst, K.: Hoberts, K.: Hatch.
390, 580-586, 1997
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A:Cross references: EMBL:236025; RID:g536487; PID:g5:6488
A Nate the scalestion anguence was subsitied to the EMBL Lata Elliusy. September
C:Genetics:
A:Map position: 2R
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R.Entian, K.D.; Koetter, F.; Rose, M.; Becker, J.; Stey, M.; Li, Z.; Wiedomann, F.; S.; Stronboln, Hedges, D.; Kissau, P.; Korol, S.; Krons, B.; Frott, M.; Stolers, submitted to the Protein September Database, August 1994

A:Reference number: $46013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 11, 865-871, 1995
A.Title. Sequence and functional analysis of a 7.2 kl DNA transcent containing four op
A:Reference number: 857353
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R:Rose, M.: Kiesau, P.: Proft, M.: Entian, K.D.
Yeast 11, 865-871, 1995
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A;Cross-references: EMHL-24-025; NU:-g538487; FID:45:0488, MIES:YERISbo
R;Baur, A.: Schaaff-Gerstenschlaeger, I.: Boles, E.: Miosga, T.: Bose, I
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A; Residues: 1-698 < ROS>
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A; Residues: 1-369 <B/
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A;Title: Sequence of a 4.8 kb fragment of Saccharomyces rerevisiae chromosomo II incl
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A; Residues: 1-698 <E
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106 TKIPENGLHNDKSI 119
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A-Title- Geromic solphics to Time dismass apin-whaste, Berrolla kurgdurferi A;Reference number: A70100, MOID:98065943

A;Recession: E7024

A;Status: preliminary: nucleic acid sequence not shown, translation not shown A;Status: preliminary: nucleic acid sequence not shown, translation not shown A;Status: preliminary: nucleic acid sequence not shown, translation not shown A;Status: preliminary: nucleic acid sequence not shown, translation not shown A;Status: 1:1146-08LEN

A;Ctoss trainers acid acid sequence strain B31
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OlSuperfamily, interlabilitial Consequence of the protein of the protei
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N.Alternate names. Nematopolate [1]

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C.Date. So Fet 1927 #Argueing_recision SC:Nov-1996 #text_change C7-New-1997

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C.Accession S18932
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C;Accession (1000) S01380

P;Maliszewski C.E. Buket, P.E. Schoenborn, M.A. Curls, B.C. Cusman, D.: Gills, Mol. Immunol. 25, 429-437, 1988

A:Tittle (Cloning, seguence and expression of bowine interleuble lealpha and interleub A;Posforonce number: A94695; Multi-gg/19652

A;Posforonce number: A94695; Multi-gg/19652

A;Accession: JL0010

A;Molecule type: mRNA
A;Posforonce number: S01, N.C. N.C. 1588
A;Title: The number: S01,80; Multi-gament, M.: Gray, P.W.

Nucleic Acids was 16, 9084, 1988
A;Title: The number: S01,80; Multi-gament, for the offNA of boving interleuble 1 beta.
A;Nocheronce number: S01,80; Multi-gament, for the offNA of boving interleuble 1 beta.
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R. Bull, C.J., While, J., Olsen, G.J., Zhou, E., Eleksdimann, E.D., Sutton, G.G., Blaider, C.J., Orthodek, B., Kirkinss, E.F., Weinster, K. M., Mirlek, J. M., Glodek, R. Silw, P. W., Hanna, M. C. Cotton, M.E., Boherts, F.M., Bulat, M.A., sain Science 273, 1058-1073, 1996
                                                      A:Molecule type: mRNA

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N;Alternate names, hematopoietin-1; IL-1 beta
C;Species, Bos primigorius taurus (cattle)
C;Species, N: Mar 1989 | spagneror remision 31 Mar 1989 | stort_change 20 Mar 1998
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